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OM protein - protein search, using sw model

Run on: June 14, 2005, 15:52:20 ; Search time 28 Seconds
(without alignments)
3207.244 Million cell updates/sec

Title: US-09-990-046A-2
 Perfect score: 6272
 Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAAATSSGNLSSRRGPGPATG 1203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

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Database :
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pcp.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pcp.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	6272	100.0	1203	3	US-09-293-505-2	Sequence 2, Appli	
2	6272	100.0	1203	4	US-09-060-939A-2	Sequence 2, Appli	
3	6248	99.6	1203	4	US-09-207-857-2	Sequence 2, Appli	
4	6248	99.6	1203	4	US-09-509-280A-2	Sequence 2, Appli	
5	5599	89.3	1182	3	US-09-293-505-7	Sequence 7, Appli	
6	5599	89.3	1182	4	US-09-060-939A-7	Sequence 7, Appli	
7	3348	53.4	1447	2	US-08-540-406-19	Sequence 19, Appl	
8	3348	53.4	1447	3	US-08-656-055-19	Sequence 19, Appl	
9	3348	53.4	1447	3	US-08-954-668-19	Sequence 19, Appl	
10	3348	53.4	1447	3	US-09-268-140-5	Sequence 5, Appli	
11	3348	53.4	1447	4	US-08-918-658-19	Sequence 19, Appl	
12	3348	53.4	1447	4	US-09-724-631-19	Sequence 19, Appl	
13	3348	53.4	1447	4	US-08-954-701A-19	Sequence 19, Appl	
14	3348	53.4	1447	5	PCF-US95-13233-19	Sequence 10, Appl	
15	3337	53.2	1434	2	US-08-540-406-10	Sequence 10, Appl	
16	3337	53.2	1434	3	US-08-656-055-10	Sequence 10, Appl	
17	3337	53.2	1434	3	US-08-954-668-10	Sequence 10, Appl	
18	3337	53.2	1434	4	US-08-918-658-10	Sequence 10, Appl	
19	3337	53.2	1434	4	US-09-724-631-10	Sequence 10, Appl	
20	3337	53.2	1434	4	US-08-954-701A-10	Sequence 10, Appl	
21	3337	53.2	1434	5	PCF-US95-13233-10	Sequence 10, Appl	
22	3048	48.6	1296	4	US-08-857-636-60	Sequence 60, Appl	
23	2627	41.9	529	3	US-09-500-063-2	Sequence 2, Appli	
24	2235	35.6	1311	2	US-08-540-406-4	Sequence 4, Appli	
25	2235	35.6	1311	3	US-08-656-055-4	Sequence 4, Appli	
26	2235	35.6	1311	3	US-08-954-668-4	Sequence 4, Appli	
27	2235	35.6	1311	4	US-08-918-658-4	Sequence 4, Appli	

ALIGNMENTS

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RESULT 1
US-09-293-505-2
; Sequence 2, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-1.
; FILE REFERENCE: P1403R1.
; CURRENT APPLICATION NUMBER: US/09/293.505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-505-2

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Query Match	100.0.0.0;	Score 6272;	DB 3;	Length 1203;
Best Local Similarity	100.0.0.0;	Pred. No. 0;		
Matches 1203;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	1	MTSPPLRELPPSYTTPARTAAPQILLAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVL	60	
QY	61	LGLLAFGALGALGRMAIETNLBQLWVEVGSRSVQELHYTKEKLGEBAAYTSQMLIQ	120	
DB	61	LGLLAFGALGALGRMAIETNLBQLWVEVGSRSVQELHYTKEKLGEBAAYTSQMLIQ	120	
QY	121	QEGENILTPPALGLHLQAALTSKQVQSVLYGKSWDLNKKIKYSGVPLIENGMIEMWIEKL	180	
DB	121	QEGENILTPPALGLHLQAALTSKQVQSVLYGKSWDLNKKIKYSGVPLIENGMIEMWIEKL	180	
QY	181	FPVCVILTPDLCPFEGAKLQGGSYLPCRDPDIQWNTLDPQOLLBELGFPASLEGREFLLDK	240	
DB	181	FPVCVILTPDLCPFEGAKLQGGSYLPCRDPDIQWNTLDPQOLLBELGFPASLEGREFLLDK	240	
QY	241	AQVGQAVYVGRPCPLHPDDLHCPCPSAPNHHSRQAPNVAHELGGCGHGF5HKFMHWQEEILLG	300	
DB	241	AQVGQAVYVGRPCPLHPDDLHCPCPSAPNHHSRQAPNVAHELGGCGHGF5HKFMHWQEEILLG	300	
QY	301	GMARDPQEGELLRAEALQSTFLMSPRLQYEHFRGDYQTHDIGWSEEQASTVLQAWQRFFV	360	
DB	301	GMARDPQEGELLRAEALQSTFLMSPRLQYEHFRGDYQTHDIGWSEEQASTVLQAWQRFFV	360	
QY	361	QLAQEALPENASQQIHAFSSTTLLDDILHAFSEVSAARVVGQYLMLLAYCVTMLRWPCAQ	420	

Db 361 QLAQALPENASQOIHFSTTLLDILHAFSEVSAARVVGGLLMLAYACVTMLRWDCAQ 420
Qy 421 SQSGVLGVLVLAVALASGLGICALLGITFNATTOVLFPFALGICVDDVFLAHAFTE 480
Db 421 SQSGVLGVLVLAVALASGLGICALLGITFNATTOVLFPFALGICVDDVFLAHAFTE 480
Qy 481 ALPGTLPQERMGECLOQTGTSTVSVLTSINNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV 540
Db 481 ALPGTLPQERMGECLOQTGTSTVSVLTSINNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVIQILPQELGDCGTVPGIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVIQILPQELGDCGTVPGIAHLTATV 600
Qy 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELSFGSTTRDLGQEBETROKAACKS 660
Db 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDPLGSELSFGSTTRDLGQEBETROKAACKS 660
Qy 661 LPCARNLAHFARYQFAPLQLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db 661 LPCARNLAHFARYQFAPLQLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRG 720
Qy 721 TKSHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHORFSSLKAVLPPPATQAPT 780
Db 721 TKSHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHORFSSLKAVLPPPATQAPT 780
Qy 781 WLHYRNWLOGIOAAFDQDQWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPDLFSOLT 840
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Db 841 TRKLVDRGLIPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
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Db 901 PAQPLEPAQPFLLRLGLOKTDVFEATEGARAAACAEAGVHAYPSGSPFLFWEQYGL 960
Qy 961 RRCFLAVALCTFLVCAALLLNPMWTAGLVLVLAMMTVELFGIMFGIKLSAIPV 1020
Db 961 RRCFLAVALCTFLVCAALLLNPMWTAGLVLVLAMMTVELFGIMFGIKLSAIPV 1020
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Qy 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPOGGG 1140
Db 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPOGGG 1140
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Db 1141 LRWGASSSLPQSFAVTTSMVAIHPPPLPGAYTHPAPDEPPSPAAATSSGNLSSRGPGP 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 2

US-09-060-939A-2
; Sequence 2, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1203 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-060-939A-2

Query Match 100.0%; Score 6272; DB 4; Length 1203;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTRSPPLRELPPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLFSLGGCIQRHCGKVL 60
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Db 61 LGLLAFGALGALGRMAIETNLQOLWVEGSRVSOELHYTKELGEEAAYTSOMLIOTAR 120
Qy 121 QEGENILTPREALGHLQAALTASKVQVSLYKGSWDLNKKICYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPREALGHLQAALTASKVQVSLYKGSWDLNKKICYKSGVPLIENGMIEMIEKL 180
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Db 181 FPCVILTPDLFCFEGAKLQGGSAYLPGRPDIQWNTLDPEOLLEELGEPASLEGFRELDDK 240
Qy 241 AQVGQAVGVRPCLHPDDLHCPSPAPNHSHRQAPNVAHELGGCHGFSKFMHWQEBELLG 300
Db 241 AQVGQAVGVRPCLHPDDLHCPSPAPNHSHRQAPNVAHELGGCHGFSKFMHWQEBELLG 300
Qy 301 GMARDPQGLLRABALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db 301 GMARDPQGLLRABALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Qy 361 QLAQALPENASQOIHFSTTLLDILHAFSEVSAARVVGGLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQALPENASQOIHFSTTLLDILHAFSEVSAARVVGGLLMLAYACVTMLRWDCAQ 420
Qy 421 SQSGVLGVLVLAVALASGLGICALLGITFNATTOVLFPFALGICVDDVFLAHAFTE 480
Db 421 SQSGVLGVLVLAVALASGLGICALLGITFNATTOVLFPFALGICVDDVFLAHAFTE 480
Qy 481 ALPGTLPQERMGECLOQTGTSTVSVLTSINNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV 540
Db 481 ALPGTLPQERMGECLOQTGTSTVSVLTSINNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVIQILPQELGDCGTVPGIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVIQILPQELGDCGTVPGIAHLTATV 600
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Qy	841	TR	KLVDBEGILIPELFYMGILTVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGCENLRIP	900
Db	841	TR	KLVDBEGILIPELFYMGILTVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGCENLRIP	900
Qy	901	PA	PLEPAQFPFLRLRGLOKQTADFEALTEGARAAACAEGAGVHAYPSPGSPFLFWEQYVGL	960
Db	901	PA	PLEPAQFPFLRLRGLOKQTADFEALTEGARAAACAEGAGVHAYPSPGSPFLFWEQYVGL	960
Qy	961	RR	CFLLAVCILLVCTFLVCALLLNPNWTAGILVILVAMTVELFGIMFGIGIKLSAIPVV	1020
Db	961	RR	CFLLAVCILLVCTFLVCALLLNPNWTAGILVILVAMTVELFGIMFGIGIKLSAIPVV	1020
Qy	1021	IL	VASVCI GYEFVTHVALGFLTTCQSSNLRAAHALEHTFAPVTDGATSTLLGLMLAGSH	1080
Db	1021	IL	VASVCI GYEFVTHVALGFLTTCQSSNLRAAHALEHTFAPVTDGATSTLLGLMLAGSH	1080
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Db	1081	FD	TVRYFFAALTIVLLTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG	1140
Qy	1141	LR	WASSSLPQSFARVTTSMTVAIHPHPLPCGAYTHPADPEPPWSPAATSSGNLSSRGPGP	1200
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; Sequence 2, Application US/09207857				
; Patent No. 6309879				
; GENERAL INFORMATION:				
; APPLICANT: Buncroft, David A.				
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED				
; TITLE OF INVENTION: THERETO				
; FILE REFERENCE: ONV-05001				
; CURRENT APPLICATION NUMBER: US/09/207,857				
; CURRENT FILING DATE: 1998-12-08				
; NUMBER OF SEQ ID NOS: 6				
; SOFTWARE: PatentIn Ver. 2.0				
; SEQ ID NO 2				
; LENGTH: 1203				
; TYPE: PRT				
; ORGANISM: human				
US-09-207-857-2				
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Best Local Similarity 99.8%; Pred. No. 0;				
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
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181	F	P	C	V	I	L	T	P	D	C	F	E	G	A	K	L	Q	G	S	A	Y	L	P	C	R	P	D	I	Q	W	T	N	L	D	P	E	Q	L	L	B	E	L	G	P	F	A	S	L	E	G	F	R	E	L	L	D	K	240	
181	F	P	C	V	I	L	T	P	D	C	F	E	G	A	K	L	Q	G	S	A	Y	L	P	C	R	P	D	I	Q	W	T	N	L	D	P	E	Q	L	L	B	E	L	G	P	F	A	S	L	E	G	F	R	E	L	L	D	K	240	
241	A	Q	V	G	Q	A	Y	V	G	R	C	L	H	P	D	D	L	H	C	P	P	S	A	P	N	H	S	R	Q	A	P	N	V	A	H	E	L	S	G	G	C	H	G	S	H	K	E	M	H	W	Q	E	L	L	G	300			
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301	G	M	A	R	D	P	Q	G	E	L	L	R	A	E	L	Q	S	T	F	L	M	S	P	R	Q	L	Y	E	H	F	G	D	Y	Q	T	H	D	I	G	W	S	E	Q	A	S	T	V	L	O	A	W	R	R	F	V	360			
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361	Q	L	A	O	E	A	L	P	E	N	A	S	Q	I	I	H	A	F	S	T	T	L	D	D	I	L	H	A	F	S	E	V	S	A	A	R	V	V	G	Y	L	L	M	L	A	Y	A	C	T	V	M	L	R	M	D	C	A	Q	420
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RESULT 3
US-09-207-857-2
; Sequence 2, Application US/09207857
; Patent No. 6309879
; GENERAL INFORMATION:
; APPLICANT: Bumcroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: human
US-09-207-857-2

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	Query Match	99.6%;	Score 6248;	DB 3;	Length 1203;	
	Best Local Similarity	99.8%;	Pred. No. 0;			
	Matches 1200;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
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Qy	1	MTRSPPLERLPSPYTPPARTAAPQILAGSLKAPLWLRAVFQGLLFSLGCGIQRHCGKVLF	60			
Db	1	MTRSPPLERLPSPYTPPARTAAPQILAGSLKAPLWLRAVFQGLLFSLGCGIQRHCGKVLF	60			
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Qy	61	LGLLAFGALGLRMAIIETNLEQLWVEVGSRSVQELHYTKEKLGEAAVTSQMLIQTAR	120			
Db	61	LGLLAFGALGLRMAIIETNLEQLWVEVGSRSVQELHYTKEKLGEAAVTSQMLIQTAR	120			
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Qy	121	QEGENILTPEALGHLLHAALTASKVQVLSLYGKSWDLNKICYKSGVP LIENGMIEMWTXL	180			

RESULT 4									
US-09-909-280A-2									
; Sequence 2, Application US/09909280A									
; Patent No. 6605700									
; GENERAL INFORMATION:									
; APPLICANT: Buncroft, David A.									
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED									
; TITLE OF INVENTION: THEREETO									
; FILE REFERENCE: CIBT-P02-050									
; CURRENT APPLICATION NUMBER: US/09/909,280A									
; PRIOR FILING DATE: 2001-07-19									
; PRIOR APPLICATION NUMBER: US 09/207,857									
; PRIOR FILING DATE: 1998-12-08									
; PRIOR APPLICATION NUMBER: US 60/067,940									
; PRIOR FILING DATE: 1997-12-08									
; NUMBER OF SEQ ID NOS: 6									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 2									
; LENGTH: 1203									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-909-280A-2									
Query Match 99.6%; Score 6248; DB 4; Length 1203;									
Best Local Similarity 99.8%; Pred. No. 0;									
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	1	MTRSPPRLRELPSPYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCQIQRHCGKVL	60						
DB	1	MTRSPPRLRELPSPYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCQIQRHCGKVL	60						
QY	61	LGLAFGALALGRLMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSQMLIQTA	120						
DB	61	LGLAFGALALGRLMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSQMLIQTA	120						
QY	121	QEGENILTPALGLHQAALTASKVQVSLYKSWDLNKKCYKSGVPLIENGMIEMIEKL	180						
DB	121	QEGENILTPALGLHQAALTASKVQVSLYKSWDLNKKCYKSGVPLIENGMIEMIEKL	180						
QY	181	FPVILTPDLPCFWEKAGLQGSAYLPGRPDIQWNTLDPEQLLELGFASLEGFRELDDK	240						
DB	181	FPVILTPDLPCFWEKAGLQGSAYLPGRPDIQWNTLDPEQLLELGFASLEGFRELDDK	240						
QY	241	AQVGQAYVGRPCLHPDDLHCPNAPNHSRQAPNVAHELSCGCHGSPKPMHWOELLIG	300						
DB	241	AQVGQAYVGRPCLHPDDLHCPNAPNHSRQAPNVAHELSCGCHGSPKPMHWOELLIG	300						
QY	301	GMARDPOGELLRAEALQSTFELMSPROLYEHPFRDGYQTHDIGWSEEQASTVLQAWORFV	360						
DB	301	GMARDPOGELLRAEALQSTFELMSPROLYEHPFRDGYQTHDIGWSEEQASTVLQAWORFV	360						
QY	361	QLAQEALPENASQOIHFASSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ	420						
DB	361	QLAQEALPENASQOIHFASSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ	420						
QY	421	SQGSVGLAGVLLVALAVASGLGICALLGITFNATTOVLFPFLAIGTGVDDVFLAHAFTE	480						
DB	421	SQGSVGLAGVLLVALAVASGLGICALLGITFNATTOVLFPFLAIGTGVDDVFLAHAFTE	480						
QY	481	ALPCTPLQERMGECLORTGTSVVLTSINNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV	540						
DB	481	ALPCTPLQERMGECLORTGTSVVLTSINNMAAFMLAALVPIPALRAFSLQAAIVVGCTFV	540						
QY	541	AVMLVFPAILSLRLRRHRCQLRDVLCFSSPCSAQVIQILPQELGDGTVPVGAHILTATV	600						
DB	541	AVMLVFPAILSLRLRRHRCQLRDVLCFSSPCSAQVIQILPQELGDGTVPVGAHILTATV	600						
QY	601	QATHTCEASSQHVVTILPPOAHLVPPSPDPLGSELSPGSGSTDLIGQEEETRQKAACKS	660						
DB	601	QATHTCEASSQHVVTILPPOAHLVPPSPDPLGSELSPGSGSTDLIGQEEETRQKAACKS	660						

RESULT 5									
US-09-293-505-7									
; Sequence 7, Application US/09293505									
; Patent No. 6348575									
; GENERAL INFORMATION:									
; APPLICANT: de Sauvage, Frederic									
; APPLICANT: Carpenter, David A.									
; TITLE OF INVENTION: Patched-2									
; FILE REFERENCE: P1405R1									
; CURRENT APPLICATION NUMBER: US/09/293,505									
; CURRENT FILING DATE: 1999-04-15									
; EARLIER APPLICATION NUMBER: US 60/081,884									
; EARLIER FILING DATE: 1998-04-15									
; NUMBER OF SEQ ID NOS: 32									
; SEQ ID NO 7									
; LENGTH: 1182									
; TYPE: PRT									
; ORGANISM: Mus musculus									
US-09-293-505-7									
Query Match 89.3%; Score 5599; DB 3; Length 1182;									
Best Local Similarity 90.9%; Pred. No. 0;									
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;									
QY	1	MTRSPPRLRELPSPYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCQIQRHCGKVL	60						
DB	1	MVRPLSIGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCIRIQHCGKVL	60						
QY	61	LGLAFGALALGRLMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSQMLIQTA	120						
DB	61	LGLVAFGALALGRLMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAYTSQMLIQTA	120						

121 QEGENILTPALGHLQAALTASKVQVSLYCKSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
121 QEGENVLTPEALDLHLQAALTASKVQVSLYCKSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
181 FPCVILTPDLPCFWEKAGLQGGSAIPLGRDPIQWNTLDPQLLELGPFPASLEGFRELDDK 240
181 FPCVILTPDLPCFWEKAGLQGGSAIPLGRDPIQWNTLDPQLLELGPFPASLEGFRELDDK 240
241 AQVQAVVGRPCPLHPDDLHCPPSPAPNHHRSQAPNVAHELGGCHGFGSHKFMHMQEELLG 300
241 AQVQAVVGRPCPLDPDDPHCPPSPAPNHHRSQAPNVAQELSGGCHGFGSHKFMHMQEELLG 300
301 GMARDPOGELLRAELAQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWORRFV 360
301 GTARDLQQLLRAELAQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASVVLQAWORRFV 360
361 QLAQALPENASQOIHAFTSTLDDILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCQA 420
361 QLAQALPENASQOIHAFTSTLDDILHAFSEVSTTRVGVGYLLMLAYACVTMLRWDCQA 420
421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
421 SQGAVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
481 ALPGTPOERMGECLORTGTSVLTSTNNMAFLMAALVPIPALRAFSLOAAIVVGCFTV 540
481 APPDTPLPERMGECLORTGTSVLTSTNNMAFLMAALVPIPALRAFSLOAAIVVGCFTV 540
541 AVMLVFPAILSLDLRRRHRQRLDLVLCFSPSCSAQVIQILPOELGDCGTPVGVIAHLTATV 600
541 AVMLVFPAILSLDLRRRHRQRLDLVLCFSPSCSAQVIQILPOELGDCGTPVGVIAHLTATV 600
601 QAPTHCBASSQHVVTLLPQAHVLPSPDPLGSELPSPGSTRDLLQGBEETRKAACKS 660
601 QAPTHCBASSQHVVTLLPQAHVLPSPDPLGSELPSPGSTRDLLQGBEETRKAACKS 660
661 LPCRARNLAHFARYQFAPLILLOSHAKAIVLVLFGALLGLSLYKATLVQDGLALTDVVPRG 720
661 LLCAMHTLAHFARYQFAPLILLOTRAKALVLLFFGALLGLSLYKATLVQDGLALTDVVPRG 720
721 TKKHAPLSAQLRYPSLYEVALVTGGFDYAHQSQALFDLHQRFSLSKAVLPPPPATQAPT 780
721 TKKHAPLSAQLRYPSLYEVALVTGGFDYAHQSQALFDLHQRFSLSKAVLPPPPATQAPT 780
781 WLHYTRNWLQIOAFAFDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
781 WLHYTRNWLQIOAFAFDQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
841 TRKLVDRREGILPPELFYMGTLTVWVSSDPLGLAASQANFYPPPPHLDKXDTTGENLRIP 900
841 TRKLVDRREGILPPELFYMGTLTVWVSSDPLGLAASQANFYPPPPHLDKXDTTGENLRIP 900
901 PAQPLEAQAQPFILRGLOKTADFVEATEGARAAEAGAGVHAYPSGSPFLWEQVYGL 960
901 PAQPLEAQAQPFILRGLOKTADFVEATEGARAAEAGAGVHAYPSGSPFLWEQVYGL 960
961 RRCFLLAVCTLLVCTFLVCAILLNPWTAGLIVLVLAMVTVELFGINGFLGKLSAIPVV 1020
961 RRCFLLAVCTLLVCTFLVCAILLNPWTAGLIVLVLAMVTVELFGINGFLGKLSAIPVV 1020
1021 ILVASVIGVEFTVHVVALGFTTQGSRLNRAAHLEHTFAPVTDGATSTLLGLMLAGSH 1080
1021 ILVASVIGVEFTVHVVALGFTTQGSRLNRAAHLEHTFAPVTDGATSTLLGLMLAGSH 1080
1081 FDFIVRFFAALTVLTLGLLHGLVLPVLLSIILGPPPEVIOMYKESPEILSPAPQGG 1140
1081 FDFIVRFFAALTVLTLGLLHGLVLPVLLSIILGPPPEVIOMYKESPEILSPAPQGG 1140
1141 LRWCASSSLPOSFARVTTMTVAHPPLPGAYTHPAPDEP 1181
1141 LRWDRPPTLQSFARVTTMTVALHPPLPGAYVHPASEEP 1181

RESULT 6
US-09-060-939A-7
; Sequence 7, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-060-939A-7

Query Match 89.3%; Score 5599; DB 4; Length 1182;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPSPYTPPARTAAQIILAGSLKAPLWLRAYFQGLLFSLGGCIQRHCGKVL 60
DB 1 MVRPLSLGELPSPYTPPARSSAPHILLAGSLQAPLWLRAYFQGLLFSLGGCIQRHCGKVL 60
QY 61 LGLAFGALGALGRMAIETNLQWVEGSRVSOELHYTKELGEEAAYTSQMLIQTAR 120
DB 61 LGLVAFGALGALGRVAVIETDLQWVEGSRVSOELHYTKELGEEAAYTSQMLIQTAR 120
QY 121 QEGENILTPALGHLQAALTASKVQVSLYCKSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
DB 121 QEGENVLTPEALDLHLQAALTASKVQVSLYCKSWDLNKKI CYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDLPCFWEKAGLQGGSAIPLGRDPIQWNTLDPQLLELGPFPASLEGFRELDDK 240
DB 181 FPCVILTPDLPCFWEKAGLQGGSAIPLGRDPIQWNTLDPQLLELGPFPASLEGFRELDDK 240
QY 241 AQVQAVVGRPCPLHPDDLHCPPSPAPNHHRSQAPNVAHELGGCHGFGSHKFMHMQEELLG 300
DB 241 AQVQAVVGRPCPLDPDDPHCPPSPAPNHHRSQAPNVAQELSGGCHGFGSHKFMHMQEELLG 300
QY 301 GMARDPOGELLRAELAQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWORRFV 360
DB 301 GTARDLQQLLRAELAQSTFLLMSPROLYEHFRGDYQTHDIGWSEEQASVVLQAWORRFV 360
QY 361 QLAQALPENASQOIHAFTSTLDDILHAFSEVSAARVGVGYLLMLAYACVTMLRWDCQA 420
DB 361 QLAQALPENASQOIHAFTSTLDDILHAFSEVSTTRVGVGYLLMLAYACVTMLRWDCQA 420
QY 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480
DB 421 SQGAVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTE 480

QY 481 ALPGTPLQRMGRCLORTGTSVVLTSINNMAAFIMAAVLPIPALRAFSLQAAIIVVGCTFV 540
Db 481 APDPTLPERMGCLASTGTSVALTSVNNMVAIFMAALVPIPALRAFSLQAAIIVGNCFA 540
QY 541 AVMLVPAIISLDLRRRHQRDLVLCFSSPCSAQVIQILPQBLGDBGTVPGIAHLTATV 600
Db 541 AVMLVPAIISLDLRRRHQRDLVLCFSSPCSAQVIQMLPQBLGDRVFPVGAHLTATV 600
QY 601 QATFCEASSQHVVTILPPOAHLVPPSPDPLGSELSPGSGTRDLGQBEETKQKAAKS 660
Db 601 QATFCEASSQHVVTILPPOAHLSPASDPLGSELSPGSGTRDLSQBEETGQQAACRP 660
QY 661 LPCARWNLAFARYQAPFAPILQSHAKAIVLVFGALLGLSLYGATLVQDGLALTDVVPRG 720
Db 661 LLCAHWTLAFARYQAPFAPILQTRAKALVLFVFGALLGLSLYGATLVQDGLALTDVVPRG 720
QY 721 TKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSSLKAVLPPPATQAPT 780
Db 721 TKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSSSLKAVLPPPATQAPT 780
QY 781 WLHYRNWLOGIOAAFDQDQWASGRITRTHSVYRNGSEGDALAYKLLIOTGDAQBPDLFSOLT 840
Db 781 WLHYRSWLQIOAAFDQDQWASGRITCHSYRNGSEGDALAYKLLIOTGNAQEPDLFSOLT 840
QY 841 TRKLVDRGLIPPELFYMGITVWVSDPLGLAASQANFYPPPEWLHDKYDTTGEMLRIP 900
Db 841 TRKLVDRGLIPPELFYMGITVWVSDPLGLAASQANFYPPPEWLHDKYDTTGEMLRIP 900
QY 901 PAQPLEFAQPFLLGLGLOKTADFEVAIEGARAACABAGQAGVHAYPSGSPFLFWEQYVGL 960
Db 901 AAQPLEFAQPFLLGLGLOKTADFEVAIEGARAACABAGQAGVHAYPSGSPFLFWEQYVGL 960
QY 961 RRCFLAVACILLVCTELVACILLNPNWTAGLIVLVAMTVLPGIMFGIIGKLSAIPVV 1020
Db 961 RRCFLAVACILLVCTELVACILLNPNWTAGLIVLVAMTVLPGIMFGIIGKLSAIPVV 1020
QY 1021 ILVASIGIGVEFVHVVALGFLTTQSGRNLRRAHALEHTAPVTDGALSTLLGLMLAGSH 1080
Db 1021 ILVASIGIGVEFVHVVALGFLTTQSGRNLRRAHALEHTAPVTDGAVTDLGLMLAGSN 1080
QY 1081 FDFIVRYFFAALVTLLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG 1140
Db 1081 FDFIIRYFFVVLVTLLGLLHGLLVPVLLSILGPPPVVQYKESQPTLNSAAQQRGG 1140
QY 1141 LRWGASSLSQSFARVTTMTVAIHPPPLPGAVIHPADPEP 1181
Db 1141 LRWDRPPTLPQSARVTTMTVALHPPPLPGAVIHPASEP 1181

RESULT 7

US-08-540-406-19
; Sequence 19, Application US/08540406
; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; Sequence 19, Application US/08540406
; Patent No. 5837538
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-540-406-19

Query Match 53.4%; Score 3348; DB 2; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.8e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFSLGCGIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAPALEQISKGKATGRKAPLWLRKAFORLLFKLGCYIQKNCCKFLVWGLLIFGA 111
QY 69 LALGLRMAIETNLEQLWVEVSRVQSELHYTKEKLGEEAAYTSQMLIQTAROEENILT 128
Db 112 FAVGLKAALETNVEELWVEVGRVSRLENTYTRQKIGEEAMFNQMLIQPKLEGANVLT 171
QY 129 PEALGHLHQAALTASQVQVSLYGVKSWDLANKICVKGVPILTIENGWIEWMIKLPCCVILTP 188
Db 172 TEALLQHLDSALQASRVHYVMYRQWKLHELCYKSGSELITETGYMQDIIEYLVPCLIIPT 231
QY 189 LDCFWEGAKLQGSAYLPGRPDIQNTNLDPEQLLEELGPPF-ASLEGFRELLEDKAAQVQAY 247
Db 232 LDCFWEGAKLQSTAYLLGKPPLRWTFDPLELEELKKINYQVDSWEEMLNKAEVGHY 291
QY 248 VGRPCLHPDDLHCPPSPAPNHHSQAPNVAHELSCGGCHGSHKFMHWQEEILLGGMARDPQ 307
Db 292 MDRPCLNPADPCDPATAPNKNSTKPLDMALVNLGCGCHGLSRKTMHWQEEILVGGTVKNST 351
QY 308 GELLRAEALQSTFLMSPRLQVYHFRG-DYOTHDIGWSBEOASTVLQAWORRRVQLAQEA 366
Db 352 GKLVSAHALQTFEQLMTQMYEHFKGYEVSH-INWEDKAAAILLEAWQRTVEVHVQS 410
QY 367 LPENASQOIHFASSTLDDILHAFSEVSAARVVGVGYLLMAYACVTMLRWDCAQSGSVG 426
Db 411 VAQNSTQKVLSTFTTTTDDILKSFSDVSIVRVASGYLLMLAYACLWMLRWDCKSKSGAVG 470
QY 427 LAGVILVALAVASGLIGCALLGITFNAATTOVLPFLALGIVGDDVDFLLAHAFTEALPG-- 484
Db 471 LAGVILVALSVAAAGLGLCLIGISFNAATTVLPFLALGVGVDDVDFLLAHAFSETGNKR 530
QY 485 TPLQERMGECLORTGTSVVLTSINNMAAFIMAAVLPIPALRAFSLQAAIIVGCTFVAVML 544
Db 531 IPFEDRTGCECLKTGTASVALTSINVTAFMAALIPIPALRAFSLQAAVIVVFNFAVLL 590
QY 545 VFPAILSLDLRRRHQRDLVLCFSSPCSAQVIQILPQBELG-----GTVPVGAIAH-- 595
Db 591 IFFAILSMDLVYRREDRLDIFCCFTSPCVSRVIOVEPQAVTDTHDNTRYSPPPPYSSHFS 650
QY 596 -----LTATVQAFTHCEASSOHVVTILPPOAHLVPPP-----SDPLGSLFSPGSGTRD 644
Db 651 AHETQITMQSTVQLRTEYDFHTHTYTAAPSEISVQPVVTVTQDTLSCSPSESTSTRD 710
QY 645 LLGOEBETKQKAAKSLPCARWNLAFARYQAPFAPILQSHAKAIVLVLFALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPEPCTKTWLTSSFAEKHYAPFLKPKAKVIVFLFLGLGLVSLYGT 768
QY 705 TLVQDGLALTDVVPRGTGKEHAFSLAQRLYFSLYEVALVTQGGFDYAHSQRALFDLHQRFS 764

Db 769 TRVRDGLDLTDIVPRETREVDFIAAQKFKYFNFYMYIVTQKA-DYPNIQHLLYDLHRSFS 827
Qy 765 SLKAVLPPPPATQAPRTWLHYRNWLOGIOAADFODWASGRITRHSYRNGSDGALAYKLL 824
Db 828 NVKVMLEENKQLPKMWLHYFRDLWQLQDAFSDWETGKIMPNYKNGSDGGLAYKLL 887
Qy 825 IOTGDAQEPDLFSQITRKLVDREGLIPPELFYMGILTVWSSDPLGLAASQAFYPPPE 884
Db 888 VQTGRDKPIDISQITKORLVDAGIINPSAFIYLTAWYNSDNDPVAYAAQANIRPHPE 947
Qy 885 WLHDKYDTTGE-NLRIPPAOPLEPAQFPFLRLGLQKTDVFEALTEGARAACABAGQAGVH 943
Db 948 WVDKADYMETRLIRIPAEPIEVAQFPFYNGLRDTSDFEALTEKRTTICSNYSYLS 1007
Qy 944 AYPGSPFLFWEQYGLRRCFLLAVALCTFLVCAALLNPNWTAGLIVLVMAMTVEL 1003
Db 1008 SYNGYFPLFWEQYGLRHLWLLFISVVLACTFLVCAVFLNPNWTAGIIVMLAMTVEL 1067
Qy 1004 FGMFGIGIKLSAIPVILVASVIGVETVHVVALGFLTTCGSRNLRAHALEHTFAPVT 1063
Db 1068 FGMGLIGIKLSAPVIVILVASVIGVETVHVVALGFLTTCGSRNLRAHALEHTFAPVT 1127
Qy 1064 DGAISTLLGLMLAGSHDFIVRYFRAALTVLTLGLLHGLVLLPVLLSILGPPPEVI-- 1121
Db 1128 DGAISTLLGLMLAGSHDFIVRYFRAALTVLTLGLLHGLVLLPVLLSILGPPPEVI-- 1187
Qy 1122 ---QMKSPSPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRAMPFGHTHSGSDSDSEVSSQTTVSGLSBELRHYEAQGA 1247
Qy 1140 G----- 1140
Db 1248 GGAHQVIVATEPNPFAHSTVHVHPSRHPPSPNPRQPHLDGSLPPGQGQPPRRDPP 1307
Qy 1141 -----LRWG-----ASSSLPQSAR 1155
Db 1308 REGMLPYLPRDFAFISTEGHSGPSNRARMPGRGARSHNPNRNPASTAMGSSVPGYQCP 1367
Qy 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITVTASVTVAVHPPVPPGPGENP 1393

RESULT 8

US-08-656-055-19
Sequence 19, Application US/08656055
Patent No. 6027882
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/540,406
FILING DATE:
ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-055-19

Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.8e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;
Qy 12 PSYTPARTAAPQILAGSL---KAPLWLRAYFQGLLFLSLGCGIQRHCKGVFLGLLAFGA 68
Db 53 PSYC-DAAFALQISKGKATGRKAPLWLRKAFQRLFLKLCYIQKNGKFLVWGLLIFGA 111
Qy 69 LALGLRMAITETNLEOLWVEVSRVSOELHYTKELGEEAAYTSOMLIQTARQGENILT 128
Db 112 FAVGLKAANLETNVEELWVEVGRVSRKELNYTRQKIGEEAAYTSOMLIQTARQGENILT 171
Qy 129 PEALGLHLOALTASKVQVSLYKSWDLNLCYKSGVPLIENGMIEMWIKLFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVMYRNQWLEHLCKYSGELITETGYMDQIIEVLYFCLITP 231
Qy 189 LDCFWEAGAKLQGSAYLPGRPDIQWNLNLPQELLEELGPF-ASLEGFRELLDKAQVOAY 247
Db 232 LDCFWEAGAKLQGSAYLPGRPDIQWNLNLPQELLEELGPF-ASLEGFRELLDKAQVOAY 291
Qy 248 VGRPCLHPDDLHCPNAPNHHSRQAPNVAHELSGCGHGFHKKFMHWOELLGLGWARDPQ 307
Db 292 MDRPCLNPDADPCPATAPNKNSTKPLDMLALVNGGCHGLSRKYMHWEEELIVGTVKNST 351
Qy 308 GELLRAEALQSTFLLMSPROLYEHFRG-DYOTHDIGWSEBQASTVLOAWORRFVQLAQEA 366
Db 352 GKLVSAHALQTMFQMTPKQMYEHFKGYEVSH-INWEDKAAALIEAKQTYEVVHQH 410
Qy 367 LPENASQIHFASSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQSQSVG 426
Db 411 VAQNSTQKVLSTTTTLLDDILKSFSDVSVIRVASGYLLMLAYACVTMLRWDCAQSQSVG 470
Qy 427 LAGVILVALAVASGIGLCALLGITFNNAATTVLPELALGIGVDDVFLLAHAFTEALPG-- 484
Db 471 LAGVILVALAVASGIGLCALLGITFNNAATTVLPELALGIGVDDVFLLAHAFTEALPG-- 530
Qy 485 TPLQERMGECLQRTGTSVLTSSINNMAAFMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
Db 531 IPEDRTGECLKRTGASVALTSINVTAFMAALIPALRAFSLQAAIVVGCTFVAVML 590
Qy 545 VFPAILSLDLRRRCORLDVLCFSSPCSAQVITQLPQELG-----GTVPVGIH-- 595
Db 591 IFFAILSMDLRYRDRRLDIFCCTSPCVSRVQVEPQAVTDTHTNTRSPPPYSSHSF 650
Qy 596 -----LTATVQAFTHCEASSQHVITLPPQAHVPPP-----SDPLGSELFPGGSTRD 644
Db 651 AHETQITMQSTVQLRTEYDPHTHYTTAEPRSEISVQPVTVTQDTLSCSPSESTSTRD 710
Qy 645 LIGQERETROKAACKSLPCARWNLHAFARYQFAPLILQSHAKAIVLVFGLLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPPTCTKWLSSFAEKHYAPFLPKPAKVVIYFLGLLGLVSLYGT 768
Qy 705 TLVQDGLALTDVVPRTGKEHAFSLAQRYFSLYEVALVTQGGFDYAHQSRALEDLHORFS 764
Db 769 TRVRDGLDLTDIVPRETREVDFIAAQKFKYFNFYMYIVTQKA-DYPNIQHLLYDLHRSFS 827
Qy 765 SLKAVLPPPPATQAPRTWLHYRNWLOGIOAADFODWASGRITRHSYRNGSDGALAYKLL 824

Db 828 NVKYMVLEENKQPKMMLHYFRDLWLOQLQDAFSDWETGKIMPNYKNGSDGGLVAYKLL 887
Qy 825 IOTGDAQEPLDLSQITRKLVDREGLIPPELFYKGLTVWSSDPLGLAASQANFYPPPE 884
Db 888 VOTGSRDKPIDISQITRKLVDREGLIPPELFYKGLTVWSSDPLGLAASQANFYPPPE 947
Qy 885 WLHDKYDTTGE-NLRIPPAQLEFAQFFPFLRLGLQKTADFEAIEGARAACAAGQAGVH 943
Db 948 WYHDKADYMPETRLRIPAAEPIYAQFFPFLRLGLQKTADFEAIEGARAACAAGQAGVH 1007
Qy 944 AYPGSGPFLFWEQYGLRRCFLAVACILLVCTFLVLCALLLNPTWAGLIVLVMAMTVEL 1003
Db 1008 SYNGYPFLFWEQYGLRHWLLFISVLACTFLVCAVFLNPTWAGLIVLVMAMTVEL 1067
Qy 1004 FGTMGFLGKLSAIPVILVASGIVGVEFTVHVALGFLITQSGRNRAAHLEHTAPVT 1063
Db 1068 FGMGLGIGKLSAVPVILVASGIVGVEFTVHVALGFLITQSGRNRAAHLEHTAPVT 1127
Qy 1064 DGAISTLLGLLMLAGSHFPIVRYFFAALTTLGLLGLHGLVLLPVLLSLTGPPPEVI-- 1121
Db 1128 DGAISTLLGLLMLAGSHFPIVRYFFAALTTLGLLGLHGLVLLPVLLSLTGPPPEVI-- 1187
Qy 1122 ----QMYKSPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVWRPMPGHTHSGSDSDSEYSSQTTVSGLSBELRHYEAQGA 1247
Qy 1140 G-----LRWG-----ASSLQPSFAR 1155
Db 1248 GGAHQVIVEATENPVFAHSTVHPSRRHPPSNRQOPHLDSGSLPPCGRQGGQRRDPP 1307
Qy 1141 -----LRWG-----ASSLQPSFAR 1155
Db 1308 REGWPLRYPRDAREFEISTEGHSGSNRARGPGRGARNPRNPASTAMGSSVPGYCQP 1367
Qy 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
Db 1368 ITTVTASVTVVAHPPPPVPGGRNP 1393

RESULT 9

US-08-954-668-19
; Sequence 19, Application US/08954668
; Patent No. 6172200
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,668
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-668-19
Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.8e-314; Indels 186; Gaps 18;
Matches 672; Conservative 203; Mismatches 285;
Qy 12 PSYTPARTAAQIILAGSL---KAPLWLRAYFOGLFLSLGCGIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAFALQISKGKATGRKAPLWLRAYFOGLFLSLGCGIQRHCGKVLFLGLLAFGA 111
Qy 69 LALGLRMAIETNLEOLWVEGSRVSOELHYKKEKIGEEAAYTSQMLIQTAROEENILT 128
Db 112 FAVGLKAANLETNVEELWVEGSRVRELNYTRQKIGEEAMFNQPMIQTPEEGANVLT 171
Qy 129 PEALGHLQAALTASKVOVSLYCKSWDLANKICVKGVPVLIENGMIEMWIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHYMYNRQWLEHLCLYKSGELITETGYMDQIIIEYLPCILITP 231
Qy 189 LDCFWEGAKLQGSAYLPGRPDIQTWNLDPQLLELGPFF-ASLEGFRELDDKAQVQAY 247
Db 232 LDCFWEGAKLQGSTAYLLCKPPLRWTFDPLELEELKKINYQVDSWEEMLNKAEVGHY 291
Qy 248 VGRCPHLPDDLHCPSPAPNHSRQAPNVAHELSGGCHGFSHKPMHWOEELLGGMARDPQ 307
Db 292 MDRPCINPADPCPATAPNKNSTKPLDMALVNLGCGHLSRKYKMHWOEELLVGTGVKNST 351
Qy 308 GELLRAELQSTFLMSPROLYEHFEG-DYQTHDICWSEEQASTVLQAMORRVLQAOEA 366
Db 352 GKLVSAHALQTFQMLTPKQMYEHFKGYEVSH-INWNEDKAAAILLEAWQRTTVEVVHVS 410
Qy 367 LPENASQOIHAFTSTLDDILHAFSEVSAARVVGGYLLMLAYACVTLMRWDCAQSGSVG 426
Db 411 VAQNSTQKVLSTFTTTLLDILKSFSDSVIRVASGYLLMLAYACVTLMRWDCSKSGAVG 470
Qy 427 LAGVLVLAVALASGLGCLALGITFNAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db 471 LAGVLVLAVALASGLGCLALGIGITFNAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 530
Qy 485 TPLQERWGECLORTGTSVVLTSINNAAFMLAALVPIPALRAFSLQAAIVGCTFVAVML 544
Db 531 IPPEDRTGELCKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAIVGCTFVAVML 590
Qy 545 VFPAILSLDLRRRCORLQVLCFCFSPCSAQVLIQLOELGD-----GTVPVGAH-- 595
Db 591 IPPAILSLDLRRRCORLQVLCFCFSPCSAQVLIQLOELGD-----GTVPVGAH-- 650
Qy 596 -----LTATVQAFTHCBASSQHVVTIIPQAHVLPVP-----SDPLGSELFPFGSGSTR 644
Db 651 AHETQITMQSTVQLRTEYDPTHTVYTTAEPSEISVQPVTVTQDTLSCSPSESTSTRD 710
Qy 645 LLQGEETRQKAACKSLPCARNLHAFARYQFAPILLQSHAKAIVLFCALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPEPCTKMTLSSFAEKHYAPFLKPKAKVYVFLFLGLGLVSLYGT 768
Qy 705 TLVQDGLALTDVVPGRGTEHAFLSAQLRYFSLYEVALVTQGGFDYAHRSQALFDLHORFS 764
Db 769 TRVRDGLDLTDIVPRETRYDFIAAQFKYFSFNWYIVTQKA-DYFNIQHLLYDLHRSFS 827
Qy 765 SLKAVLPPPATQAPRTWLYHRYNWLQGIQAAPDQDQWASGRITRHSYNGSEDEGALYKLL 824
Db 828 NVKYMVLEENKQPKMMLHYFRDLWLOQLQDAFSDWETGKIMPNYKNGSDGGLVAYKLL 887
Qy 825 IOTGDAQEPLDLSQITRKLVDREGLIPPELFYKGLTVWSSDPLGLAASQANFYPPPE 884
Db 888 VOTGSRDKPIDISQITRKLVDREGLIPPELFYKGLTVWSSDPLGLAASQANFYPPPE 947
Qy 885 WLHDKYDTTGE-NLRIPPAQLEFAQFFPFLRLGLQKTADFEAIEGARAACAAGQAGVH 943

Db 948 WVDKADYMPETRLRIIPAAEIEYAQPFYVGLNGLEDTSDFEAEIEKVRTICSNYTSGLS 1007
Qy 944 AYPGSGPFLWEQYGLRRCFLAVACILLVCTFLVCAALLINPWTAGLIVLVLAMTVL 1003
Db 1008 SYPNGYPFLWEQYGLRHWLLLSFVSVLACTFLVCAVFLNPNWTAGIIVVVLALMTVEL 1067
Qy 1004 FGIMFGIGIKLSAIPVVLVASVGIGVEFTVHVHVALGFLTTQGSNRLRAHALEHTFAPVT 1063
Db 1068 FGMGLIGIKLSAIPVVLVASVGIGVEFTVHVHVALGFLTTQGSNRLRAHALEHTFAPVT 1127
Qy 1064 DGAISTLLGLMLAGSHDFDFTVRYFFAALTVLTLLGLHGLVLLPVLLSILGPPEVI-- 1121
Db 1128 DGAISTLLGLMLAGSHDFDFTVRYFFAALTVLTLLGLHGLVLLPVLLSILGPPEVI-- 1187
Qy 1122 ---QMKESPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRFAMPFGHTHSGSDSDSEYSSQTTVSGLSEELRHYEAQGA 1247
Qy 1140 G-----LRWG-----ASSSLPQSFA 1140
Db 1248 GGAHQVIVEATENPVFAHSTVHPEGRHPPSNRQPHLDSGLPPGQOQPRRDP 1307
Qy 1141 -----LRWG-----ASSSLPQSFA 1155
Db 1308 REGWPLPYRRDAPFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQ 1367
Qy 1156 VTT-----SMTVAIHPPLPGAYIHP 1176
Db 1368 ITTWTASVTVAVHPPVPGGRNP 1393

RESULT 10

US-09-268-140-5
; Sequence 5, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRCR, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; PRIOR FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-268-140-5

Query Match 53.4%; Score 3348; DB 3; Length 1447;
Best Local Similarity 49.9%; Pred. No. 1.8e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

Qy 12 PSYTPPARTAPOILAGSL---KAPLWLRAYFQGLFSLGCGIORHCKVFLGLAFGA 68
Db 53 PSYC-DAFALEQISKGKATGRKAPLWLRKAFORLLFKLGCYIOKNCCKFLVGLLIFGA 111
Qy 69 LALGLRMAIETNLEQLWVEGSRVSOBELHYTKELGEEAAAYTSQMLIQTARQGENILT 128
Db 112 FAVGLKAANLETVNEELWVEGSRVRELNTYTRQKIGEEAMFNQMLIQTPEKGANVLT 171
Qy 129 PEALGLHLQAALASKQVSVLYGKSWDLNKTKYSGVPLIENGMIEMIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHYVYNNRWKLEHLCKYSGELITETGYMDQIIIEYLPCLITP 231
Qy 189 LDCFEWAKLOGGSAYLPCRDIQWNTNLDPQLLEELGFP-ASLEGFRELLDKAQGOAY 247
Db 232 LDCFEWAKLOGSTAYLLGKPLRTNFPDLEFLESELKKNYQVDSWEEMLNKAQVGHY 291

Qy 248 VGRPCLHPDDLHCPPSAPNHHHSROAPNVAHELSCGCHGFSHKPMHQBELLGGMARDPQ 307
Db 292 MDRPCLNPAEDCDPATAPNKNSTKPLDMALVNLGCHGCHLSKRYMHQBELLVGGTVKNST 351
Qy 308 GELLARALOSTFLMSPROLYEHEFRG-DYOTDIGHWSEEQASTVLOAQWRRFVQLAQEA 366
Db 352 KLVSAHALQTMFQMTPKQYEHFKGYEVYSH-INNEDKAAALILEAWQTYVEVYHQS 410
Qy 367 LPENASQIHFASSTLLDDILHAFSEVSAARVWGGYLLMLAYACVTMLRWDCAQSGSVG 426
Db 411 VAQNSTQKVSFTTTTLLKSPSDSVIRVASGYLLMLAYACLTLMLRDCSKSQGAVG 470
Qy 427 LAGVLLVALAVASGLGICALLGITFNAAATQVLFALGIGVDVDFLLAHAFTEALPG-- 484
Db 471 LAGVLLVALSVAAAGLGLCSLIGISFNAAATQVLFALGIGVDVDFLLAHAFSEGTQNK 530
Qy 485 TPLQERMGECLORTGTSVLTSTINMAAFMAALVPIPALRAFSLQAAIVGCTFVAVML 544
Db 531 IPEDRTGECCLKRTGASVALTSISNVTAFMAALIPALRAFSLQAAVVVVFAMVLL 590
Qy 545 VFPAILSLDLRRRHCRDLVLCFSPSCSAQVILPQELGD-----GTVPVGIAH-- 595
Db 591 IFPAILSMDLVRRDRDLDFCCPTSPCVSRVIQVEPOAYTDTHDNTRYSPPPYSSHSF 650
Qy 596 -----LTATVQAFTHCEASSQHVVTILPQAHLVPPP-----SDPLGSELFSFGSTRD 644
Db 651 AHETQITMQSTQVLRTEYDPHTHYVYTTABRSEISVQPVTVTQDTLSCQSESTSTRD 710
Qy 645 LLGOEBETROKAAACKSLPCARNLHAFAFYQAFAPLLQSHAKAIVLVFGLALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPEPCTKNTLSSFAEKHYAFLKPKAKVVVIFLFLGLGVSILGT 768
Qy 705 TLVQDGLALTVDVPRGTHKHAFLSAQLRFSLYEVALVTCGGFDYAHYSQRALFDLHQRF 764
Db 769 TRVEDGLDLTDIVPERETREYDFIAAQFKYFSEYNNVITVTKA-DYPNIQHLLYDLHRSFS 827
Qy 765 SLKAVLPPATQAPRTWLHYRNWLOGIOAAPDOOWASGRITRHSYRNGSDEGALAYKLL 824
Db 828 NVKYMLEENKQLPKMHLHFRDLWLOGLODAFSDWETGKIMPNNNYKNGSDGVLAYKLL 887
Qy 825 IOTGDAQBLDFSLQTLTKLVDRGLIPPELFFYMGTLVWVSSDPLGLAASQANFYPPPE 884
Db 888 VQTGSRDKPIDISQTLTKQLVDADGIINPSAFYIYLTAWNSNDPVAYAASQANTRPHPE 947
Qy 885 WLHDKYDTTGE-NLRIPPAQPLEPAQFPFLRGLQKTADFVEAIEGARAACAAGQAGVH 943
Db 948 WVDKADYMPETRLRIIPAAEIEYAQPFYVGLNGLEDTSDFEAEIEKVRTICSNYTSGLS 1007
Qy 944 AYPGSGPFLWEQYGLRRCFLAVACILLVCTFLVCAALLINPWTAGLIVLVLAMTVL 1003
Db 1008 SYPNGYPFLWEQYGLRHWLLLSFVSVLACTFLVCAVFLNPNWTAGIIVVVLALMTVEL 1067
Qy 1004 FGIMFGIGIKLSAIPVVLVASVGIGVEFTVHVHVALGFLTTQGSNRLRAHALEHTFAPVT 1063
Db 1068 FGMGLIGIKLSAIPVVLVASVGIGVEFTVHVHVALGFLTTQGSNRLRAHALEHTFAPVT 1127
Qy 1064 DGAISTLLGLMLAGSHDFDFTVRYFFAALTVLTLLGLHGLVLLPVLLSILGPPEVI-- 1121
Db 1128 DGAISTLLGLMLAGSHDFDFTVRYFFAALTVLTLLGLHGLVLLPVLLSILGPPEVI-- 1187
Qy 1122 ---QMKESPE-----ILSP-----APQGG 1139
Db 1188 NGLNRLPTSPPEPPSVVRFAMPFGHTHSGSDSDSEYSSQTTVSGLSEELRHYEAQGA 1247
Qy 1140 G-----LRWG-----ASSSLPQSFA 1140
Db 1248 GGAHQVIVEATENPVFAHSTVHPEGRHPPSNRQPHLDSGLPPGQOQPRRDP 1307
Qy 1141 -----LRWG-----ASSSLPQSFA 1155
Db 1308 REGWPLPYRRDAPFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMGSSVPGYCQ 1367
Qy 1156 VTT-----SMTVAIHPPLPGAYIHP 1176

RESULT 13

US-08-954-701A-19
 ; Sequence 19, Application US/08954701A
 ; Patent No. 6610507
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley, Hoag & Eliot
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII(text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/954,701A
 ; FILING DATE: 20-OCT-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36709
 ; REFERENCE/DOCKET NUMBER: SUV-003.08
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1447 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-954-701A-19

Query Match 53.4%; Score 3348; DB 4; Length 1447;
 Best Local Similarity 49.9%; Pred.No. 1.8e-314;
 Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAAPQILAGSL---KAPLWLRAYFQGLLFLSGCGIQRHCGKVLFLGLLAFGA 68
 DB 53 PSYC-DAAPALEQISKGATGRKAPLWLRKAFQRLFLKLCYIQKNCGRFLVVGLLIFGA 111
 QY 69 LAIGLRMAIETNLEQLWVEVGRSVQELHYTKEKIGEEAAVTSQMLIQARQGENILT 128
 DB 112 FAVGLKAAANLETVNVEELWVEVGRSVRELNYTRQKIGEEAMFNPQLMIQPKKEGANVLT 171
 QY 129 PEALGHLOALTASKVOVSLYCKSDLNKICVYKGVPLLENGMIEMIEKLPCCVILTP 188
 DB 172 TEALLQHLQALQASRVHVYTMNRQWLEHLCYKSGELITETGYMDIOIIBLYPLCLITP 231
 QY 189 LDCFWGAKLQGSAYLPGRPDIQWNLDPQLELLELGPFF-ASLEGFRELLEDKAQQVQAY 247
 DB 232 LDCFWGAKLQSGTAVILGKPPRLRWTFDPLELEELKKINYQVDSWEEMLNKAEVGHGY 291
 QY 248 VGRPCLHDDLHCPSPAPNHSQAPNVAHELGGCHGFSKFMWQBELLLCGMARDPQ 307
 DB 292 MDRPCLNPADPCPATAPNKNSTKPLDMLVNLGCGCHLSRKYMHQBELIVGCTVKNST 351
 QY 308 GELLREALELQSTFLMSPROLYEHERFG-DYQTHDIGWSEBQASTVLQAWORRRFVQLAQEA 366
 DB 352 GKUVSAHALQTMFLQMLTPKQMYEHFYGVTVSH-INWEDKAAALILEAWORTVVEVHHQS 410
 QY 367 LPENASQQIHAFSSTLDDILHAFSEVSAARVVGGVLLMLAYACVTMLRWDCAQSGSVG 426

DB 411 VAQNSTQKVLSTFTTTTDDILKSFSDSVIRVASGYLLMLAYACVTMLRWDCSKSQGAVG 470
 QY 427 LAGVLAVAVASGLGICALLGHTENAAATTOVLPELALGIGVDDVFLLAHAFTEALPG-- 484
 DB 471 LAGVLLVALSVAAAGLGLCSLIGISFNAATTQVLPFLALGVDDVFLLAHAFSETGNKR 530
 QY 485 TPLQERMGECLORTGTSSVLTISNNMAAFMAALVPIPALRAFSLQAAIIVVGCTFVAVML 544
 DB 531 IPFEDRTGECLEKXTGASVALTSISNTAFPMALIPALRAFSLQAAVNVVFNFAVLL 590
 QY 545 VFPAILSLDLRRRCORLDVLCFSSPSCSAQVITQILPQELGD-----GTVPVGAH-- 595
 DB 591 IFFAILSMDLRYRDRRLDIFCCFTSPCVSRVIOVEPQAYTDTHDNTRYSPPPYSSHFS 650
 QY 596 -----LTATVQAFTHCEASSQHVVTILPQAHLYPPP-----SDPLGSLFLSPGSTRD 644
 DB 651 AHETQITMQSTVOLRTEYDPHTHTYTAEPRESEISVQPVVTQDTLSCOSPESTSTRD 710
 QY 645 LLQBEETRQKAAACKSLPCARWNLAHFARYQFAPLQLQSHAKAIVLVLFGALLGLSLYGA 704
 DB 711 LLSQFSDS--SLHCLPEPCTKWTLSFAEKHYAPFLKPKAKVVVIFLFLGLLGVSLYGT 768
 QY 705 TLVQDGLALTVDVVPRTGKEHAFLSAQLRYPSLYEVALVTQGGPDYAHSQBALFDLHQFHS 764
 DB 769 TRVRDGLDLTDIVPRETREYDFIAAQKYPFSFYNMIVITQKA-DYPNIQHLHYDLHRSFS 827
 QY 765 SLKAVLPAPATQAPRTWLYHYRNWLOGIOAAFDODWASGRIHRSYRNSEDCALAYKLL 824
 DB 828 NVKVMLEENKQLPKWMLHYFRDMLQGLQADQFOSDMWETGKIMPNNYKNGSDGGLAYKLL 887
 QY 825 IOTGDAQEPLDFSQLTRKLVDREGIIPPELFYMWGLTVVSSDPLGLAASQANFYPPPE 884
 DB 888 VQTGSRDKPIDISQLTKQRLVDADGIINPSAFIYLTAWVNDPVAYAASQANIRHPPE 947
 QY 885 WLHDKYDTTGE-NLRIPPAQLEFAQFPFLRLQKLTADFVEAIEGARAAACABAGQGVH 943
 DB 948 WVHDKADYMPETRLRIPAAEPIEYQFPFYVGLNGLRDTSDPVEAIEKVRTICSNVTSIGLS 1007
 QY 944 AYPSSGPELFWEOYLGRLRCFLAVCILAVCTELVCAALLNNEWTAGLIVLVLAMMTVEL 1003
 DB 1008 SYPNGYFFLFWEOYIGLRHLLLFISVVLACTFLVCVAVLNNPWTAGIIVVVLALMTVEL 1067
 QY 1004 FGIMGFLGKLSAIPVVLVAVSGVIGVEFTHVALGFLTTQGSRLNRAHALEHTFAPVT 1063
 DB 1068 FGMMGLIGIKLSAVPVVILLIASVIGVEFTHVALAFLTAIGDKNRRAVLALEHMFAPVL 1127
 QY 1064 DGAISTLLGLLMLAGSHDFIVRYFPAALTIVTLGLLHGLVLLPVLLSILGPPPEVI-- 1121
 DB 1128 DGAVSTLLGLVLMAGSEDFIVRYFPAVLAAILTILVGLNGLVLLPVLSPFGPYPEVSPA 1187
 QY 1122 ----QMKESPE-----ILSPP-----APQGG 1139
 DB 1188 NGLNRLPTSPPEPPSVVRFPMPGHTHSGSDSSDSEYSSQTTVTVSGLSBELRHYEQQA 1247
 QY 1140 G-----LRWG----- 1140
 DB 1248 GGPQHVIIVEATENPVFAHSTVHVPSRHHPPSNPRQPHLDGSLUPPGRQGOQPRDPP 1307
 QY 1141 -----LRWG-----ASSLSPOSFAR 1155
 DB 1308 REGWLPPLYRPRRDAFEISTEGHSGPSNRARMGPRGARSHNPRNPASTAMGSSVPGYQCP 1367
 QY 1156 VTT-----SMTVAIHPPPLPGAVIHP 1176
 DB 1368 ITTVTASVTVAVHPPPPVPGGRNP 1393

RESULT 14
 PCT-US95-13233-19
 ; Sequence 19, Application PC/TUS9513233
 ; GENERAL INFORMATION:
 ; APPLICANT: THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY

```

; TITLE OF INVENTION: Patched Genes and their Use
;
; NUMBER OF SEQUENCES: 19
;
; CORRESPONDENCE ADDRESS:
; ADDRESS: Flehr, Hombach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
;

```

Query Match 53.4%; Score 3348; DB 5; Length 1447;
Best Local Similarity 49.9%; Pred. NO. 1.8e-314;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

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Qy	189	LDCFWEGAKLQGSAYLFGRPDIOWTNLDPQLLEELGPF-ASLEGPRELLDKAUVQAY	247
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Qy	367	LPENASQOIHAFSSTTTDDLIILHAFSEVSARVVGYYLLMLAYACTWMLRWDCAOSQ	426
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 07:58:06 ; Search time 46 Seconds
(without alignments)

1952.235 Million cell updates/sec

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Perfect score: 1203

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1203	100.0	1203	4	US-09-060-939A-2
3	900	74.8	1203	3	US-09-207-857-2
4	900	74.8	1203	4	US-09-909-280A-2
5	497	41.3	529	3	US-09-500-063-2
6	94	7.8	1182	3	US-09-293-505-7
7	94	7.8	1182	4	US-09-060-939A-7
8	43	3.6	46	3	US-09-500-063-4
9	15	1.2	1296	4	US-08-857-636-60
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11	15	1.2	1434	3	US-08-656-055-10
12	15	1.2	1434	3	US-08-954-668-10
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14	15	1.2	1434	4	US-09-724-631-10
15	15	1.2	1434	4	US-08-954-701A-10
16	15	1.2	1434	5	PCT-US95-13233-10
17	15	1.2	1447	2	US-08-540-406-19
18	15	1.2	1447	3	US-08-656-055-19
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21	15	1.2	1447	4	US-08-918-658-19
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9	0.7	11	2	US-08-540-406-8	Sequence 8, Appl
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9	0.7	209	4	US-09-270-767-41607	Sequence 41607, A
9	0.7	336	4	US-09-270-767-41511	Sequence 41511, A
9	0.7	1285	2	US-08-540-406-6	Sequence 6, Appl
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9	0.7	1285	4	US-09-724-631-6	Sequence 6, Appl
9	0.7	1285	4	US-08-954-701A-6	Sequence 6, Appl
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9	0.7	1286	3	US-09-268-140-3	Sequence 3, Appl
9	0.7	1299	3	US-08-460-900C-62	Sequence 62, Appl
9	0.7	1299	3	US-08-674-509B-48	Sequence 48, Appl
9	0.7	1299	3	US-08-954-698-48	Sequence 48, Appl
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9	0.7	1299	4	US-09-448-188-48	Sequence 48, Appl
9	0.7	1299	4	US-08-954-128-48	Sequence 48, Appl
9	0.7	1299	4	US-08-954-740-48	Sequence 48, Appl
9	0.7	1311	2	US-08-540-406-4	Sequence 4, Appl
9	0.7	1311	3	US-08-656-055-4	Sequence 4, Appl
9	0.7	1311	3	US-08-954-668-4	Sequence 4, Appl
9	0.7	1311	4	US-08-918-658-4	Sequence 4, Appl
9	0.7	1311	4	US-09-724-631-4	Sequence 4, Appl
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9	0.7	1311	5	PCT-US95-13233-4	Sequence 4, Appl
8	0.7	76	3	US-09-293-505-4	Sequence 4, Appl
8	0.7	76	4	US-09-060-939A-4	Sequence 4, Appl
8	0.7	117	4	US-09-248-796A-16571	Sequence 16571, A
8	0.7	149	4	US-09-270-767-37985	Sequence 37985, A
8	0.7	149	4	US-09-270-767-53202	Sequence 53202, A
8	0.7	157	4	US-09-252-991A-20823	Sequence 20823, A
8	0.7	176	4	US-09-216-393B-73	Sequence 73, Appl
8	0.7	243	4	US-09-252-991A-29870	Sequence 29870, A
8	0.7	420	4	US-09-543-681A-6289	Sequence 6289, Ap
8	0.7	531	3	US-09-380-420C-2	Sequence 2, Appl
8	0.7	531	4	US-09-899-642A-2	Sequence 2, Appl
8	0.7	548	2	US-08-468-576B-19	Sequence 19, Appl
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8	0.7	979	4	US-09-015-399-5	Sequence 5, Appl
8	0.7	1003	4	US-09-949-016-11260	Sequence 11260, A
8	0.7	1411	4	US-09-252-991A-23628	Sequence 23628, A
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7	0.6	9	3	US-09-186-170-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1

US-09-293-505-2

; Sequence 2, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P140SKI
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-293-505-2

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121	QEGENILTPALGHLQAALTASKVQVSLYKSKWDLNKI CYKSGVPLIENGMIEMWIEKL	180
Qy	181	FPVILTPDCFWGAKLOGGSAYLPGRPDIQTNLDPQLLELPGFASLEGPRELLDK	240
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Qy	361	QLAQEALPENASQOIHAFSSTLDDILHAFSEVSAARVVGYYLMLAYACVTMLRW	420
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SEQUENCE CHARACTERISTICS:

LENGTH: 1203 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-09-060-939A-2

Query Match 100.0%; Score 1203; DB 4; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	LGLLAFGALALGLRMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAVTSQMLIQ	120
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Qy	361	QLAQEALPENASQOIHAFFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLR	420
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Db	601	QAEHCEASSQHVVTILPPOAHVLPSPDPLGSELSPGSGSTRDLICQEBETRQK	660
Qy	661	LPCARWNLAHFARYQFAPLLQSHAKAIVLVFGLALGLSLYGATLVQDGLALTDV	720
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Db	781	WLHYRNWLOGIQAAFPDQWASGRIITHSYRNSEDCALAYKLLIQTQDAQEB	840
Qy	841	TRKLVDREGILIPPELFYMGILTVMVSSDPLGLAASQANFYPPPEWLHDKYD	900
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RESULT 3

US-09-207-857-2
; Sequence 2, Application US/09207857
; Patent No. 6309879

GENERAL INFORMATION:

; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; FILE REFERENCE: ONV-05001
; CURRENT APPLICATION NUMBER: US/09/207,857
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: human
US-09-207-857-2

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy	61	LGLLAFGALALGLRMAIETNLEQLWVEGSRVSOELHYTKEKLGEEAAVTSQMLIQ	120
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Qy	121	QEGENILTPALGLHLQAALTASKVQVSLYCKSWDLNKKIYKSGVPLIENGMIEMIEKL	180
Db	121	QEGENILTPALGLHLQAALTASKVQVSLYCKSWDLNKKIYKSGVPLIENGMIEMIEKL	180
Qy	181	FPVCILTPDLDFWEGAKLOGGSAYLPGRPDQIQTNLDPQLLELGFASLEGFREL	240
Db	181	FPVCILTPDLDFWEGAKLOGGSAYLPGRPDQIQTNLDPQLLELGFASLEGFREL	240
Qy	241	AQVGOAVVGRPCPLHDPDLHCPSPAPNHHSRQAPNVAHELGGCHGFSHKPMHWOELL	300
Db	241	AQVGOAVVGRPCPLHDPDLHCPSPAPNHHSRQAPNVAHELGGCHGFSHKPMHWOELL	300
Qy	301	GMARDPQGLLRAEALQSTFLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWOR	360
Db	301	GMARDPQGLLRAEALQSTFLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWOR	360
Qy	361	QLAQEALPENASQOIHAFFSSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLR	420
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Db 541 AVMLVFPAILSLDLRRRHQORLDVLCFFSPCSAQVIQILPQELGDTGTVPGIAHLTATV 600
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QY 961 RRCFLLAVCILVCTFLVCALLLNPMWAGLIVLVLAMWTVELFGIMFGIGIKLSAIPV 1020
Db 961 RRCFLLAVCILVCTFLVCALLLNPMWAGLIVLVLAMWTVELFGIMFGIGIKLSAIPV 1020
QY 1021 ILVASVGIGVEFTVHVALGFLTQGSRNRAAAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVGIGVEFTVHVALGFLTQGSRNRAAAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
QY 1081 PDFIVRYFFAALTIVTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG 1140
Db 1081 PDFIVRYFFAALTIVTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGG 1140
QY 1141 LRWGASSSLPQSFARVTTSMTVAIHPPLPGAYTHPADRPWPSPAATSSGNLSSRGPGP 1200
Db 1141 LRWGASSSLPQSFARVTTSMTVAIHPPLPGAYTHPADRPWPSPAATSSGNLSSRGPGP 1200
QY 1201 ATG 1203
Db 1201 ATG 1203
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```
RESULT 4
US-09-909-280A-2
; Sequence 2, Application US/09909280A
; Patent No. 6605700
; GENERAL INFORMATION:
; APPLICANT: Bumcrott, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-280A-2

Query Match 74.8%; Score 900; DB 4; Length 1203;
Best Local Similarity 99.8%; Pred.No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRSPPLRELPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLFLSLGCGIORHCGKVL 60
Db 1 MTRSPPLRELPSYTPPARTAAPQIILAGSLKAPLWLRAYFQGLLFLSLGCGIORHCGKVL 60
QY 61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRSQBELHYTKELGEEAAYTSQMLIQTAR 120
Db 61 LGLLAFGALALGLRMAIIETNLEQLWVEVGSRSQBELHYTKELGEEAAYTSQMLIQTAR 120
QY 121 QEGENILTPENALGLHIQAALTASKVOVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPENALGLHIQAALTASKVOVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDLCFMEGAKLQGGSAAYLPGRPDIQWTNLDPEQLLEELGPFASFLEGFRELLDK 240
Db 181 FPCVILTPDLCFMEGAKLQGGSAAYLPGRPDIQWTNLDPEQLLEELGPFASFLEGFRELLDK 240
QY 241 AQVQAYVGRPCPLHPDDLHCPSPAPNHHSRQAPNVAHELSCGCHGFSHKFMHQEELLG 300
Db 241 AQVQAYVGRPCPLHPDDLHCPSPAPNHHSRQAPNVAHELSCGCHGFSHKFMHQEELLG 300
QY 301 GMARDPQGLLRAREALOSTFELMSPROLYEHFEGDYQTHDIGWSEQAQSTVLQAWORRFV 360
Db 301 GMARDPQGLLRAREALOSTFELMSPROLYEHFEGDYQTHDIGWSEQAQSTVLQAWORRFV 360
QY 361 QLAQAEALPENASQOIHAFSSTLLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQAEALPENASQOIHAFSSTLLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
QY 421 SQSVGLAGVLLVALAVASGLGICALLGITFNAAATQTVLPFLALGICGVDDVFLLAHAFT 480
Db 421 SQSVGLAGVLLVALAVASGLGICALLGITFNAAATQTVLPFLALGICGVDDVFLLAHAFT 480
QY 481 ALPGTLPQERMGECLOQTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAAIVVGCFTV 540
Db 481 ALPGTLPQERMGECLOQTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAAIVVGCFTV 540
QY 541 AVMLVFPAILSLDLRRRHQORLDVLCFFSPCSAQVIQILPQELGDTGTVPGIAHLTATV 600
Db 541 AVMLVFPAILSLDLRRRHQORLDVLCFFSPCSAQVIQILPQELGDTGTVPGIAHLTATV 600
QY 601 QAETHCEASSQHVVTILPPOAHLVPPSPDLGSELSPGSTRDLGQEEETQKAACKS 660
Db 601 QAETHCEASSQHVVTILPPOAHLVPPSPDLGSELSPGSTRDLGQEEETQKAACKS 660
QY 661 LPCARWNLAHFARYQAPALLQSHAKAIVLVLFAGLLGLSLYGATLVQDGLALTDVVPRG 720
Db 661 LPCARWNLAHFARYQAPALLQSHAKAIVLVLFAGLLGLSLYGATLVQDGLALTDVVPRG 720
QY 721 TKEHAFLSAQLRYFSLYEVALVTQGGPDYAHSQRALFDLHQRFSSSLKAVLPPPATQAPRT 780
Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGPDYAHSQRALFDLHQRFSSSLKAVLPPPATQAPRT 780
QY 781 WLHYRNLWLOGIOAAFPDQDQWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPIDFSOLT 840
Db 781 WLHYRNLWLOGIOAAFPDQDQWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPIDFSOLT 840
QY 841 TRKLVDRREGILPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRREGILPPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
QY 901 PAQPLEFAQPFLLRGLQKTADFVEATEGARAAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
Db 901 PAQPLEFAQPFLLRGLQKTADFVEATEGARAAACAEAGQAGVHAYPSGSPFLFWEQYLGL 960
```

Db 901 PAQPLEFAQPFLRLGLQKTADFVEAIEGARAAACAGQAGVHAYPSGSPFLFWEQYGL 960
Qy 961 RRCFLAVCTILLVCTFLVCALLLNPMWTAGLIVLVLAMMTVELFGIMFGIKLSAIPVV 1020
Db 961 RRCFLAVCTILLVCTFLVCALLLNPMWAGLIVLVLAMMTVELFGIMFGIKLSAIPVV 1020
Qy 1021 ILVASVIGVEFTVHVALGFLTTCGSRNLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVIGVEFTVHVALGFLTTCGSRNLRAAHLEHTFAPVTDGAISTLLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALTIVTLGLLHGLVLPVLLSILGPPPEVIOMYKESPEILSPAPOGG 1140
Db 1081 FDFIVRYFFAALTIVTLGLLHGLVLPVLLSILGPPPEVIOMYKESPEILSPAPOGG 1140
Qy 1141 LRWGASSLSQSFARVTTSTMTVAIHPPPLPGAYIHPADPPMSPAAATSSGNLSSRGPGP 1200
Db 1141 LRWGASSLSQSFARVTTSTMTVAIHPPPLPGAYIHPADPPMSPAAATSSGNLSSRGPGP 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 5
US-09-500-063-2
; Sequence 2, Application US/09500063
; Patent No. 6353092
; GENERAL INFORMATION:
; APPLICANT: David P. Kelsell
; APPLICANT: Michael R. Barnes
; APPLICANT: Tania Tamson Testa
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30311-D1
; CURRENT APPLICATION NUMBER: US/09/500,063
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 529
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-500-063-2

Query Match 41.3%; Score 497; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 497; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 491 MGECLQRTGTSVVLTSINNMAAFMLAALVPIPALRAPSLQAAIVVGTFFVAVMLVFPAIL 550
Db 1 MGECLQRTGTSVVLTSINNMAAFMLAALVPIPALRAPSLQAAIVVGTFFVAVMLVFPAIL 60
Qy 551 SLDLRRHRCORLDVLCFSSPCSAQVTOILPOELGDGTVPVGTIAHLTATVQAEHTCEASS 610
Db 61 SLDLRRHRCORLDVLCFSSPCSAQVTOILPOELGDGTVPVGTIAHLTATVQAEHTCEASS 120
Qy 611 QHVVTILPPOAHLVPPSPDLGSELFPGGSTRDLLGOEBETROKKAACKSLPCARNLH 670
Db 121 QHVVTILPPOAHLVPPSPDLGSELFPGGSTRDLLGOEBETROKKAACKSLPCARNLH 180
Qy 671 FARYQFAPLLQSHAKAIVLVLFGALGLSLYGATLVQDGLATDVVPRGTKEHAFSLAQ 730
Db 181 FARYQFAPLLQSHAKAIVLVLFGALGLSLYGATLVQDGLATDVVPRGTKEHAFSLAQ 240
Qy 731 LRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSSLKAVLPPATQAPRTWLHYRNWQ 790
Db 241 LRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSSLKAVLPPATQAPRTWLHYRNWQ 300
Qy 791 GIOAQPDDWASGRITRHSYRNSEDGALAYKLLIQTGDQEPDLDFSQLTKLVDRGL 850
Db 301 GIOAQPDDWASGRITRHSYRNSEDGALAYKLLIQTGDQEPDLDFSQLTKLVDRGL 360
Qy 851 IPPELFYMGTLVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIPPAQPLEFAQF 910

Db 361 IPPELFYMGTLVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIPPAQPLEFAQF 420
Qy 911 PFLLRGLQKTADFVEAIEGARAAACAGQAGVHAYPSGSPFLFWEQYGLRRCFLAVCI 970
Db 421 PFLLRGLQKTADFVEAIEGARAAACAGQAGVHAYPSGSPFLFWEQYGLRRCFLAVCI 480
Qy 971 LLVCTFLVCALLLNPM 987
Db 481 LLVCTFLVCALLLNPM 497

RESULT 6
US-09-293-505-7
; Sequence 7, Application US/09293505
; Patent No. 6348575
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/293,505
; CURRENT FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: US 60/081,884
; EARLIER FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
; LENGTH: 1182
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-293-505-7

Query Match 7.8%; Score 94; DB 3; Length 1182;
Best Local Similarity 100.0%; Pred. No. 1.8e-79;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 693 FGALLGLSLYGATLVQDGLATDVVPRGTKEHAFSLAQRLYFSLYEVALVTQGGFDYAH 752
Db 693 FGALLGLSLYGATLVQDGLATDVVPRGTKEHAFSLAQRLYFSLYEVALVTQGGFDYAH 752
Qy 753 ORALFDLHORFSSSLKAVLPPATQAPRTWLHYR 786
Db 753 ORALFDLHORFSSSLKAVLPPATQAPRTWLHYR 786

RESULT 7
US-09-060-939A-7
; Sequence 7, Application US/09060939A
; Patent No. 6709838
; GENERAL INFORMATION:
; APPLICANT: Frederic de Sauvage, David A. Carpenter
; TITLE OF INVENTION: Patched-2
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,939A
; FILING DATE: 15-Apr-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1405
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-060-939A-7
Query Match 7.8%; Score 94; DB 4; Length 1182;
Best Local Similarity 100.0%; Pred. No. 1.8e-79;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 693 FGALLGLSLYGATLVQDGLALTDVVRGTTKEHAFLSAQLRYFSLYEVALVTQGGFDYVH 752
Db 693 FGALLGLSLYGATLVQDGLALTDVVRGTTKEHAFLSAQLRYFSLYEVALVTQGGFDYVH 752

Qy 753 QRALFDLHORFSSLKAVLPBPATQAPRTWLHYR 786
Db 753 QRALFDLHORFSSLKAVLPBPATQAPRTWLHYR 786

RESULT 8
US-09-500-063-4
; Sequence 4, Application US/09500063
; Patent No. 6353092
; GENERAL INFORMATION:
; APPLICANT: David P. Kelsell
; APPLICANT: Michael R. Barnes
; APPLICANT: Tania Tamson Testa
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30311-D1
; CURRENT APPLICATION NUMBER: US/09/500,063
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 46
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-500-063-4

Query Match 3.6%; Score 43; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 488 QERMGECQLRTGTSVVLTSINNMAFLMALVPIPALRAFSLQ 530
Db 4 QERMGECQLRTGTSVVLTSINNMAFLMALVPIPALRAFSLQ 46

RESULT 9
US-08-857-636-60
; Sequence 60, Application US/08857636
; Patent No. 6552181
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael Carlton
; APPLICANT: Hahn, Heidi Eve
; APPLICANT: Wicking, Carol
; APPLICANT: Christiansen, Jeffrey
; APPLICANT: Zaphiropoulos, Peter G.
; APPLICANT: Gailani, Mae R.
; APPLICANT: Shanley, Susan Mary
; APPLICANT: Chidambaram, Abirami
; APPLICANT: Vorechovsky, Igor
; APPLICANT: Holmberg-Lindstrom, Erika
; APPLICANT: Uden, Anne Birgitte
; APPLICANT: Gillies, Susan Alana
; APPLICANT: Negus, Kylie
; APPLICANT: Smyth, Ian Mcleod
; APPLICANT: Pressman, Carol Leah
; APPLICANT: Leffell, David J.
; APPLICANT: Gerrard, Bernard
```

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; APPLICANT: Goldstein, Alisa Miriam
; APPLICANT: Mainwright, Brandon
; APPLICANT: Toftgard, Rune Carl-Magnus
; APPLICANT: Chenevix-Trench, Georgia
; APPLICANT: Bale, Allen E.
; TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/857,636
; FILING DATE: 16-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,906
; FILING DATE: 17-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P00011
; FILING DATE: 21-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU P00363
; FILING DATE: 07-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,765
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tcm
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-278200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1296 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1296
; OTHER INFORMATION: /note= "amino acids encoded by human
; OTHER INFORMATION: nevold basal cell carcinoma syndrome
; OTHER INFORMATION: (NECCS) (PATCHED (PTC)) cDNA"
;
US-08-857-636-60
Query Match 1.2%; Score 15; DB 4; Length 1296;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLFALG 465
Db 344 FNAATTQVLPLFALG 358

RESULT 10
US-08-540-406-10
; Sequence 10, Application US/08540406
; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
```

APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,406
FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-540-406-10

Query Match 1.2%; Score 15; DB 2; Length 1434;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

RESULT 11
US-08-656-055-10
Sequence 10, Application US/08656055
Patent No. 6027882
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,055
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/540,406
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-656-055-10
Query Match 1.2%; Score 15; DB 3; Length 1434;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

RESULT 12
US-08-954-668-10
Sequence 10, Application US/08954668
Patent No. 6172200
GENERAL INFORMATION:
APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched Genes and their Use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,668
FILING DATE: 20-Oct-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36709
REFERENCE/DOCKET NUMBER: SUV-003.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1434 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-954-668-10

Query Match 1.2%; Score 15; DB 3; Length 1434;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

Db 481 FNAATTQVLPFLALG 495

RESULT 13

US-08-918-658-10

; Sequence 10, Application US/08918658

; Patent No. 6429354

; GENERAL INFORMATION:

; APPLICANT: SCOTT, MATHEW P

; GOODRICH, LISA V

; JOHNSON, RONALD L

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/918,658

; FILING DATE: 22-Aug-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/656,055

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/540,406

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: a60190-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1434 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-08-918-658-10

Query Match 1.2%; Score 15; DB 4; Length 1434;

Best Local Similarity 100.0%; Pred. No. 6.5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPFLALG 465

Db 481 FNAATTQVLPFLALG 495

RESULT 14

US-09-724-631-10

; Sequence 10, Application US/09724631

; Patent No. 6551782

; GENERAL INFORMATION:

; APPLICANT: SCOTT, MATHEW P

; GOODRICH, LISA V

; JOHNSON, RONALD L

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

Qy 451 FNAATTQVLPFLALG 465

Db 481 FNAATTQVLPFLALG 495

RESULT 15

US-08-954-701A-10

; Sequence 10, Application US/08954701A

; Patent No. 6610507

; GENERAL INFORMATION:

; APPLICANT: SCOTT, MATHEW P

; GOODRICH, LISA V

; JOHNSON, RONALD L

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley, Hoag & Eliot

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/954,701A

; FILING DATE: 20-OCT-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36709

Qy 451 FNAATTQVLPFLALG 465

Db 481 FNAATTQVLPFLALG 495

Query Match 1.2%; Score 15; DB 4; Length 1434;

Best Local Similarity 100.0%; Pred. No. 6.5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPFLALG 465

Db 481 FNAATTQVLPFLALG 495

RESULT 15

US-08-954-701A-10

; Sequence 10, Application US/08954701A

; Patent No. 6610507

; GENERAL INFORMATION:

; APPLICANT: SCOTT, MATHEW P

; GOODRICH, LISA V

; JOHNSON, RONALD L

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley, Hoag & Eliot

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/954,701A

; FILING DATE: 20-OCT-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36709

; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-701A-10

Query Match 1.2%; Score 15; DB 4; Length 1434;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

RESULT 16

PCT-US95-13233-10
; Sequence 10, Application PC/TUS9513233
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US

ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13233
; FILING DATE: 06-OCT-1990
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13233-10

Query Match 1.2%; Score 15; DB 5; Length 1434;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

RESULT 17

US-08-540-406-19
; Sequence 19, Application US/08540406

; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-540-406-19

Query Match 1.2%; Score 15; DB 2; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 18

US-08-656-055-19
; Sequence 19, Application US/08656055
; Patent No. 6027882
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,055
; FILING DATE:

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/540,406
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-055-19

Query Match 1.2%; Score 15; DB 3; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 19
US-08-954-668-19
; Sequence 19, Application US/08954668
; Patent No. 6172200
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,668
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-668-19

Query Match 1.2%; Score 15; DB 3; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 20
US-09-268-140-5
; Sequence 5, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-268-140-5

Query Match 1.2%; Score 15; DB 3; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 21
US-08-918-658-19
; Sequence 19, Application US/08918658
; Patent No. 6429354
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,658
; FILING DATE: 22-Aug-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,055
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:

```


TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-08-918-658-19

Query Match 1.2%; Score 15; DB 4; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 22
US-09-724-631-19
; Sequence 19, Application US/09724631
; Patent No. 6551782
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,631
FILING DATE: 28-Nov-6551782-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/656,055
FILING DATE: 1996-05-31
APPLICATION NUMBER: 08/540,406
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-398-3249
TELEFAX: 415-781-1989

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-724-631-19

Query Match 1.2%; Score 15; DB 4; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 23
US-08-954-701A-19
; Sequence 19, Application US/08954701A
; Patent No. 6610507
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,701A
FILING DATE: 20-OCT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36709
REFERENCE/DOCKET NUMBER: SUV-003.08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-954-701A-19

Query Match 1.2%; Score 15; DB 4; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 24
PCT-US95-13233-19
; Sequence 19, Application PC/TUS9513233
; GENERAL INFORMATION:
; APPLICANT: THE BOARD OF TRUSTEES OF TEH LELAND STANFORD JUNIOR UNIVERSITY
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/13233
;; FILING DATE: 06-OCT-1990
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rowland, Bertram I
;; REGISTRATION NUMBER: 20015
;; REFERENCE/DOCKET NUMBER: a60190-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-781-1989
;; TELEFAX: 415-398-3249
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1447 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US95-13233-19

Query Match 1.2%; Score 15; DB 5; Length 1447;
Best Local Similarity 100.0%; Pred. No. 6.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509
|||||

RESULT 25
US-08-540-406-11
; Sequence 11, Application US/08540406
; Patent No. 5837538
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-540-406-11

Query Match 0.7%; Score 9; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 TPLDCFWEG 195
Db 3 TPLDCFWEG 11
|||||

RESULT 26
US-08-656-055-11
; Sequence 11, Application US/08656055
; Patent No. 6027882
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,055
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/540,406
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-656-055-11

Query Match 0.7%; Score 9; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 TPLDCFWEG 195
Db 3 TPLDCFWEG 11
|||||

RESULT 27
US-08-954-668-11
; Sequence 11, Application US/08954668
; Patent No. 6172200
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,668
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-954-668-11

Query Match 0.7%; Score 9; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 TPLDCFWEG 195
Db 3 TPLDCFWEG 11

RESULT 28
US-08-918-658-11
; Sequence 11, Application US/08918658
; Patent No. 6429354
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,658
; FILING DATE: 22-Aug-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,055
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-918-658-11

Query Match 0.7%; Score 9; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 TPLDCFWEG 195
Db 3 TPLDCFWEG 11

RESULT 29
US-09-724-631-11
; Sequence 11, Application US/09724631
; Patent No. 6551782
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. 6551782-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-724-631-11

Query Match 0.7%; Score 9; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 TPLDCFWE 195
3 TPLDCFWE 11

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1  RESULT 30
2  US-08-954-701A-11
3  ; Sequence 11, Application US/08954701A
4  ; Patent No. 6610507
5  ; GENERAL INFORMATION:
6  ; APPLICANT: SCOTT, MATHEW P
7  ; APPLICANT: GOODRICH, LISA V
8  ; APPLICANT: JOHNSON, RONALD L
9  ; TITLE OF INVENTION: Patched Genes and their Use
10 ; NUMBER OF SEQUENCES: 19
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Foley, Hoag & Eliot
13 ; STREET: One Post Office Square
14 ; CITY: Boston
15 ; STATE: MA
16 ; COUNTRY: USA
17 ; ZIP: 02109
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: ASCII(text)
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/954,701A
25 ; FILING DATE: 20-OCT-1997
26 ; CLASSIFICATION: 435
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: Vincent, Matthew P.
29 ; REGISTRATION NUMBER: 36709
30 ; REFERENCE/DOCKET NUMBER: SUV-003.08
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: 617-832-1000
33 ; TELEFAX: 617-832-7000
34 ; INFORMATION FOR SEQ ID NO: 11:
35 ; SEQUENCE CHARACTERISTICS:
36 ; LENGTH: 11 amino acids
37 ; TYPE: amino acid
38 ; STRANDEDNESS: single
39 ; TOPOLOGY: linear
40 ; MOLECULE TYPE: peptide
41 US-08-954-701A-11

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Query Match          0.7%; Score 9; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 9: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 187 TPLDCFWE 195
db 3 TPLDCFWE 11

Search completed: June 16, 2005, 08:09:44
Job time : 50 secs


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Db 121 QEGENILTPALGLHLQAALTASKVQVSLYKGSWDLNKKCYKSGVPLIENGMIEMIEKL 180
Qy 181 FPCVILTPDLFCFEGAKLQGSAYLPCRDPDIQNTNLDPEQLLEELGPFASLEGFRELDDK 240
Db 181 FPCVILTPDLFCFEGAKLQGSAYLPCRDPDIQNTNLDPEQLLEELGPFASLEGFRELDDK 240
Qy 241 AQVQAYVGRPCVLCVHPPDLHCPSPAPNHHSQAQPNVAHELSSGGCHGFSHKFMHQEELLG 300
Db 241 AQVQAYVGRPCVLCVHPPDLHCPSPAPNHHSQAQPNVAHELSSGGCHGFSHKFMHQEELLG 300
Qy 301 GWARDPQELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db 301 GWARDPQELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Qy 361 QLAQEAALPENASQOIHAFSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTLMLRWDCAQ 420
Db 361 QLAQEAALPENASQOIHAFSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTLMLRWDCAQ 420
Qy 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLLAHAFTE 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLLAHAFTE 480
Qy 481 ALPGTLPQERMGECLQRTGTSVVLTSINNMAAFILMAALVPIPALRAFSLQAAIIVVGCTFV 540
Db 481 ALPGTLPQERMGECLQRTGTSVVLTSINNMAAFILMAALVPIPALRAFSLQAAIIVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVQIILPQELGDTVPVGIHAHTATV 600
Db 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVQIILPQELGDTVPVGIHAHTATV 600
Qy 601 QAFTHCEASSQHVVTILPQAHILVPPSPDLPLGSELSPGSGSTRDLLGQEBEETKQAACKS 660
Db 601 QAFTHCEASSQHVVTILPQAHILVPPSPDLPLGSELSPGSGSTRDLLGQEBEETKQAACKS 660
Qy 661 LPCARNLNAHFARYQFAPLQLQSHAKAIVLVLFGALLGLSLYGATLVQDGLATDVVPRG 720
Db 661 LPCARNLNAHFARYQFAPLQLQSHAKAIVLVLFGALLGLSLYGATLVQDGLATDVVPRG 720
Qy 721 TKEHAFSLAQLRFSLYEVALVTCGGFDYAHSORALFDLHORFSSLKAVLPPATQAPRT 780
Db 721 TKEHAFSLAQLRFSLYEVALVTCGGFDYAHSORALFDLHORFSSLKAVLPPATQAPRT 780
Qy 781 WLHYRNWLQGIQAAFPQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Db 781 WLHYRNWLQGIQAAFPQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLT 840
Qy 841 TRKLVDRGLIPPELFYMGTLTVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGTLTVWSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQPFLLRGLQKTADFVEATEGARACAEAGQAGVHAYPSGSPFLFWEQVYGL 960
Db 901 PAQPLEFAQPFLLRGLQKTADFVEATEGARACAEAGQAGVHAYPSGSPFLFWEQVYGL 960
Qy 961 RRCFLLAVCILLVCTFLVCAALLNPMTAGLIVLVLAMTVLFGIMFGIGIKLSAIPVV 1020
Db 961 RRCFLLAVCILLVCTFLVCAALLNPMTAGLIVLVLAMTVLFGIMFGIGIKLSAIPVV 1020
Qy 1021 ILVASVIGVEFTVHVVALGFTTQGSNRLRAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVIGVEFTVHVVALGFTTQGSNRLRAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
Qy 1081 FDFIVRYFFAALTVLTLGLHLGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPOGGG 1140
Db 1081 FDFIVRYFFAALTVLTLGLHLGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPOGGG 1140
Qy 1141 LRWGASSSLPQSFARVTTMTVAIHPPPLPGAYIHPADPEPPWSPATSSGNLSSRGPGP 1200
Db 1141 LRWGASSSLPQSFARVTTMTVAIHPPPLPGAYIHPADPEPPWSPATSSGNLSSRGPGP 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203
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RESULT 2

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US-09-909-280A-2
; Sequence 2, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Bumcrot, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THEREFO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-280A-2
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Query Match 99.6%; Score 6248; DB 9; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 1 MTRSPPLRELPPSYTPPARTAAPQIILAGSLKAPLMLRAYPQGLLFSLGGCQIQRHCGKVL 60
Db 1 MTRSPPLRELPPSYTPPARTAAPQIILAGSLKAPLMLRAYPQGLLFSLGGCQIQRHCGKVL 60
Qy 61 LGLLAFGALALGRMAIIETNLQOLMVEGSRVQSEILHYTKELGEEAAVTSQMLQIOTAR 120
Db 61 LGLLAFGALALGRMAIIETNLQOLMVEGSRVQSEILHYTKELGEEAAVTSQMLQIOTAR 120
Qy 121 QEGENILTPALGLHLQAALTASKVQVSLYKGSWDLNKKCYKSGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPALGLHLQAALTASKVQVSLYKGSWDLNKKCYKSGVPLIENGMIEMIEKL 180
Qy 181 FPCVILTPDLFCFEGAKLQGSAYLPCRDPDIQNTNLDPEQLLEELGPFASLEGFRELDDK 240
Db 181 FPCVILTPDLFCFEGAKLQGSAYLPCRDPDIQNTNLDPEQLLEELGPFASLEGFRELDDK 240
Qy 241 AQVQAYVGRPCVLCVHPPDLHCPSPAPNHHSQAQPNVAHELSSGGCHGFSHKFMHQEELLG 300
Db 241 AQVQAYVGRPCVLCVHPPDLHCPSPAPNHHSQAQPNVAHELSSGGCHGFSHKFMHQEELLG 300
Qy 301 GWARDPQELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Db 301 GWARDPQELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASTVLQAWQRRFV 360
Qy 361 QLAQEAALPENASQOIHAFSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTLMLRWDCAQ 420
Db 361 QLAQEAALPENASQOIHAFSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTLMLRWDCAQ 420
Qy 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLLAHAFTE 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDVFLLAHAFTE 480
Qy 481 ALPGTLPQERMGECLQRTGTSVVLTSINNMAAFILMAALVPIPALRAFSLQAAIIVVGCTFV 540
Db 481 ALPGTLPQERMGECLQRTGTSVVLTSINNMAAFILMAALVPIPALRAFSLQAAIIVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVQIILPQELGDTVPVGIHAHTATV 600
Db 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPCSAQVQIILPQELGDTVPVGIHAHTATV 600
Qy 601 QAFTHCEASSQHVVTILPQAHILVPPSPDLPLGSELSPGSGSTRDLLGQEBEETKQAACKS 660
Db 601 QAFTHCEASSQHVVTILPQAHILVPPSPDLPLGSELSPGSGSTRDLLGQEBEETKQAACKS 660
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Qy	661	LPCARNWLNHPARVQFAPLILLOSHAKAIVLVFLGALLGLSLYGATVIVQDGLALTDVVPRG	720
Db	661	LPCARNWLNHPARVQFAPLILLOSHAKAIVLVFLGALLGLSLYGATVIVQDGLALTDVVPRG	720
Qy	721	TKHAFPLSAQLRYFSLYEVALVTOGGFDYAHQSORALFDLHORFSSLKAVLPPPPATQAPRT	780
Db	721	TKHAFPLSAQLRYFSLYEVALVTOGGFDYAHQSORALFDLHORFSSLKAVLPPPPATQAPRT	780
Qy	781	WLHYRNWLOGIOAAFQODWASGRITRHSYRNGSEGDGALAYKLLIQTGDAQEPLDFSOLT	840
Db	781	WLHYRNWLOGIOAAFQODWASGRITRHSYRNGSEGDGALAYKLLIQTGDAQEPLDFSOLT	840
Qy	841	TRKLVDR EGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDVTTCENLRIP	900
Db	841	TRKLVDR EGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDVTTCENLRIP	900
Qy	901	PAQPLEFAQPPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPGSPFLFWEQYLGL	960
Db	901	PAQPLEFAQPPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPGSPFLFWEQYLGL	960
Qy	961	RRCPELLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMTVLFGIMFGIFGIKLSAIPVV	1020
Db	961	RRCPELLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMTVLFGIMFGIFGIKLSAIPVV	1020
Qy	1021	ILVASVGIGVEFTVHVVALGFLTTCGSRNLRAAHALEHTFAPVTDGALSTLLGLMLAGSH	1080
Db	1021	ILVASVGIGVEFTVHVVALGFLTTCGSRNLRAAHALEHTFAPVTDGALSTLLGLMLAGSH	1080
Qy	1081	FDFTVRYFFAALTVLTLGLLHGLVLLPVLSSILGPPPEVIQMYKESPEILSPAPQGGG	1140
Db	1081	FDFTVRYFFAALTVLTLGLLHGLVLLPVLSSILGPPPEVIQMYKESPEILSPAPQGGG	1140
Qy	1141	LRWGASSLSQSFARVTTMTVAIHPPPLPGAYIHPADDEPPWSPAATSSGNLSSRGPGP	1200
Db	1141	LRWGASSLSQSFARVTTMTVAIHPPPLPGAYIHPADDEPPWSPAATSSGNLSSRGPGP	1200
Qy	1201	ATG 1203	
Db	1201	ATG 1203	
RESULT 3			
US-09-990-046-7			
; Sequence 7, Application US/09990046			
; Patent No. US20020156245A1			
; GENERAL INFORMATION:			
; APPLICANT: de Sauvage, Frederic			
; APPLICANT: Carpenter, David A.			
; TITLE OF INVENTION: Patched-2			
; FILE REFERENCE: P1405R1			
; CURRENT APPLICATION NUMBER: US/09/990,046			
; CURRENT FILING DATE: 2001-11-20			
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505			
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15			
; NUMBER OF SEQ ID NOS: 32			
; SEQ ID NO 7			
; LENGTH: 1182			
; TYPE: PRT			
; ORGANISM: Mus musculus			
US-09-990-046-7			
Query Match 89.3%; Score 5599; DB 9; Length 1182;			
Best Local Similarity 90.9%; Pred. No. 0;			
Matches 1074; Conservative 43; Mismatches 64; Indels 0; Gaps 0;			
Qy	1	MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPILWLFRAYFQGLLFSIGCGIORHCKGVLF	60
Db	1	MVRPLSIGELPPSYTPPARSSAPHILAGSLQAPLWLFRAYFQGLLFSIGCRIKHCKGVLF	60
Qy	61	LGLLAFGALALGLRMAIETNLEOLWVEGSRVSOELHYHTEKELGEBAAVTSQMLIQTAR	120
Db	61	LGLVAFGALALGRVAIETDLEOLWVEGSRVSOELHYHTEKELGEBAAVTSQMLIQTAH	120

RESULT 4

US-08-954-701A-19
; Sequence 19, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; FILING DATE: 20-OCT-1997
; APPLICATION NUMBER: US/08/954,701A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-701A-19

Query Match 53.4%; Score 3348; DB 8; Length 1447;
Best Local Similarity 49.9%; Pred. No. 7.9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSTYPTARTAAQILAGSL---KAPLWLRAYFQGLLFLSLGCGIQRHCGKVLFLGLLAFGA 68
DB 53 PSYC-DAAFALQISKGATGRKAPLWLRKAFQRLFLKLCYIQKNGKFLVYVGLLIIFA 111

QY 69 LALGLRWAITETLEQLWVEVGRVSQELHYTKELGEERAYTSQMLIOTARQGENILT 128
DB 112 FAVGLKAANLETNVEELWVEVGRVSELNYYTRQKIGERAMFQPMIOTPFKEEGANVLT 171

QY 129 PEALGLHQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIEMWIEKLPFCVILTP 188
DB 172 TEALLQHLDSALQASRVHVYVYRWQWLEHLCKYKSELITETGYMQIIEYLPCLIIPT 231

QY 189 LDCFWGAKLQGSAYLPGRPDITQWNLNDEQLLEELGPF-ASLEGFRELDDKAQVQAY 247
DB 232 LDCFWGAKLQGTAVLLGKPLRLWTNFDPLEFLEELKKNLYQVDSWEEMLNKAEVGHY 291

QY 248 VGRPCLHPDDLCPSPNPHHSQAPNVAHELGGCHGPFKFWHQEELLGLGMARDPQ 307
DB 292 MDRPCLNPADPCPATAPNKNSTKPLDMALVNLGCGHLSRKYNHMQEELIVGGTVKNST 351

QY 308 GELLRAELQSTLLMSPROLYEHFRG-DYQTHDIDGWSEQAQSTVLAQWRRFVQLAQEA 366
DB 352 GKLVSAHALQTMQLTPKQMYEHFKGYEVVSH-INWNEDKAAALAEAWQTYVEVHQ 410

QY 367 LPENASQIHFASSTLDDILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQSGSVG 426
DB 411 VAQNSTQKVLSTTTTLLDILKSFSDSVIRVASGYLLMLAYACLTMLRWDCKSKQAVG 470

QY 427 LAGVLLVALAVASGLGICALLGITFNAATTQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
DB 471 LAGVLLVALSVAAGLGLCSLIGISFNAAATTQVLPFLALGVDDVFLLAHAFSETGNKR 530

QY 485 TPLQERMGECLORTGTSVVLTSTNNMAAFMAALVIPALRAFSLOAAIIVGCTTFVAVML 544
DB 531 IPFEDRTGECLEKRTGASVALTSTSNVTAFFMAALIIPALRAFSLOAAVVFVNFAMVLL 590

QY 545 VPPAIIISLDLRRHRCORLDVLCFSPSCSAOVIIQLPOELGD-----GTVPVGAH-- 595
DB 591 IFFAILSMOLYRREDRLDIFCCFTSPCVSRVUQVEPOATDTHDTRVSRPPPYSSHSP 650

QY 596 -----LATATQAFTHCEASSQHVVITLPPQAHVLP--SDPLGSELPSPGSTRD 644
DB 651 AHETQITMQSTVQLRTEYDPHTHYVYTTAEPRSEISVQPVTVTQDTLSCQSPSTSTRD 710

QY 645 LLQGEETQKAAKSLPCARNLHAHPARYQFAPLLQSHAKAIVLVFQALLGLSLYGA 704
DB 711 LLSQFSDS--SLHCLPEPPCTKWTLSFAEKHAPFLLKPKAKVWVIFLFLGLLGSVLYGT 768

QY 705 TLVQDGLALTQVVPRGCTKEHAFLSAOLRYFSLVEVALVTQGGFDYAHQSORALFDLHORPS 764
DB 769 TRVRDGLDLTDIVPRETRYDFIAAQKFYSFTNMYIVTQKA-DYFNIQHLLYDLHRSPS 827

QY 765 SLKAVLPPPATQAPRTWLHYRNWLOGIQAAAFQDQDWASGRITRHSYRNGSESGALAYKLL 824
DB 828 NVKYMVLEENKQLPKMWLHYFRDLQGLQDAFDSQWETGKIMENNYKNGSDGGLAYKLL 887

QY 825 IQGDAQEPLDFSQLTRKLVOREGLIPPELFYMGJTVWVSSDPLGLAASQANFYPPPE 884
DB 888 VQTGSRDKPIDISQLTQKRLVDADGIIINFSAFYILTAWVNSDPVAYAAASQANIRHPRE 947

QY 885 WLHDKYDTTGE-NLRTPPAQPLEFAQFPFLIRGLQKTADFEVAIEGARAACAAGQGVH 943
DB 948 WVHDKADYMPETRLRIPAAEPIEYAQFPFLNGLRDTSDFEVAIEKVRTICSNYTSIGLS 1007

QY 944 AVPSGPFPLFWEQYLGRLRCFLIACVILLVCTFLVCALLILNPNWTAGLIIVLVLAMMTVEL 1003
DB 1008 SYENGYPFLFWEQYIGLRHLLLFISVLACTFLVCVFLNPNWTAGIIVMLALMTVEL 1067

QY 1004 FGIMGFLGIKLSAIPVILVASVIGIVETVHVVALGFLTTQSGRNLRRAHALHHTFAPVT 1063
DB 1068 FGMGLIGIKLSAIPVILIASVIGIVETVHVVALAFLTAIGDKNRRVALALEHMFAPVL 1127

QY 1064 DGAISTLLGLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLPVLSTILGPPPEVI-- 1121
DB 1128 DGAIVSTLLGLMLAGSEDFIVRYFFAVLAILTLGLVNLGLVLLPVLSPFFGYPEVSPA 1187

QY 1122 ---QWKEESPE-----ILSP-----APQGG 1139
DB 1188 NGLNRLPTTSPPEPPSVVRPAMPPTHSGSDSDSEYSSQTTVSGLSEELRHVEAQGA 1247

QY 1140 G----- 1140
DB 1248 GGPQHVVIVEATENPVFAHSTVVHPESRHHPPSNRQPHLDSCGLPPGCGQQRDRDP 1307

QY 1141 -----LRWG-----ASSSI PQSFAR 1155
DB 1308 REGMLPPLVRRDAPFEISTEGHSGPSNRARWGPGRGASHNPNRNPASTAMGSSVPGYCQ 1367

QY 1156 VTT-----SMTVAIHPPPLPGAYIHP 1176
DB 1368 ITTVIASASVTVAHPPVPGGPNP 1393

RESULT 5

US-09-898-533-5
; Sequence 5, Application US/09898533
; Patent No. US20020106656A1
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.

;; TITLE OF INVENTION: TRC9, A GENE RELATED TO THE HEDGEHOG RECEPTOR,

;; TITLE OF INVENTION: PATCHED

;; FILE REFERENCE: 93445-00004

;; CURRENT APPLICATION NUMBER: US/09/898,533

;; CURRENT FILING DATE: 2001-07-02

;; PRIOR APPLICATION NUMBER: US/09/268,140

;; PRIOR FILING DATE: 2000-03-12

;; NUMBER OF SEQ ID NOS: 46

;; SOFTWARE: Patent in Ver. 2.0

;; SEQ ID NO 5

;; LENGTH: 1447

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; US-09-898-533-5

Query Match 53.4%; Score 3348; DB 9; Length 1447;

Best Local Similarity 49.9%; Pred. No. 7.9e-267;

Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSYTPPARTAQAQLAGSL---KAPLMIRAYFQGLLSLGGGIGQIRHCGKVLFLGLLAFGA 68
 DB 53 PSYC-DAAPALAEQISKSGATKATKAPLWLRKAFORLLFLKGLCYQKNGKFLVGLLIFGA 111
 QY 69 LALGLRMAITETNLEQLWVEGSRVSOELHYTKEKIGEEAAYTSOMLIQTAROREGNILT 128
 DB 112 FAVGLKAANLETNVEELWVEGSRVSELNFTYRKIGEEAAYTSOMLIQTAROREGNILT 171
 QY 129 PEALGLHQAALTASKQVQSLYKGSWDLNLCIKYSGVPLIENGMIEMIKLPCVILTP 188
 DB 172 TEALLQHLDSALQASRVHVMYKQWLEHLKCYSGELITETGYMDQIIEVLYPCLITP 231
 QY 189 LDCFWGAKLQGSAYLPGRPDIOWNLDPQLLEELGPF-ASLEGFRELLDQAQVQAY 247
 DB 232 LDCFWGAKLQSGTAYLLGKPLRWNTNFDPLELEELKKNINYQVDSWEEMLNKAEVGHY 291
 QY 248 VGRPLHPDDILHCPPSNHSHRQAPNVAHELSCGCHFSKPMHWQELLGGMARDPQ 307
 DB 292 MDRPCLNPADPCPATAPNKNSTKPLDMALVINGGCHLSRKYMHQWQELIVGTGKNST 351
 QY 308 GELLRAEALQSTFLMSPROLYHFRG-DYOTHDIGMSEBQASTVLOAWRRFVQLAQA 366
 DB 352 GKLVSALQTMQMTQKPMQYEHFKGYEVSH-INWNEKKAALAEAWQRTYEVVHQ 410
 QY 367 LPENASQIIFAFSTLDDILHAFSEVSAARVGVGGLLMLAYACVTLRWDCQSQSGV 426
 DB 411 VAQNSTQKVSFTTTTLLDKSPDSVIRVASGYLLMLAYACLTLRWDCSKSQGAVG 470
 QY 427 LAGVLLVALAVASGLIGCALLGITFNAAATTOVLPLFALGIGVDDVFLLAHAFALPG-- 484
 DB 471 LAGVLLVALSVAAGLGLCSLIGISFNAATTOVLPLFALGIGVDDVFLLAHAFSETGQNK 530
 QY 485 TPLQERMGECLORTGTSVLTINNMAAFMAALVPIPALRAFSLQAAIVVGCTFVAVML 544
 DB 531 IPEDRTGECLORTGASVALTSISNTAFMAALIPALRAFSLQAAIVVVFAMVLL 590
 QY 545 VFPAILSLDLRRHRCORLDVLCFSPSCSAQVILQPELGD-----GTVPVGAIAH-- 595
 DB 591 IFPAILSMVLYRREDRLDFCCFTSPCVSRVQVEPQAVTDHNTNRYSPPPYSSHSF 650
 QY 596 -----LTATVQAFTHCEASSQHVVILPQAHVPPP-----SDPLGSELFPFGGSTRD 644
 DB 651 AHETQITMQSTVQLRTYDPTHVYTTABPRSEISVQPVTVTQDTLSCQSPSESTSTRD 710
 QY 645 LLGQEBETRQKAAKSLPCARNWLAHFAFYQFAPLLAQSHAKAIVLFLGALLGLSLYGA 704
 DB 711 LLSQFSDS--SLHCLPEPCTKWTLSFPAEKYAPFLKPKAKVWVIFFLGLGVSLYGT 768
 QY 705 TLVDGGLADVVPRGKHAFLSAQLRYSLSYVALVTOGGFDYAHQSRAFLDHLHRSFS 764
 DB 769 TRVRDGLDLDIVPRETFREYDFINAAQKYSFYNNYIVTQKA-DYPNIQHLLDLHRSFS 827
 QY 765 SLKAVLPPPTAQPTRWLHYRNWNLQIGQAFQODWASGRITHRSYNGSEDEGALAYKLL 824

DB 828 NVKVMLEENKQLPKMWLHYFRDWLQLODAFSDMWTGKIMPNYKNGSDGVLAYKLL 887
 QY 825 IQGDAQEPLDFSQLTTRKLVLDREGILPPELFTVWVSSDPLGLAASQANFYPPPE 884
 DB 888 VQTGSRDKPIDISQLTQKRLVDADGIINPSAFYILYLTAWVNDPVAASQANIRPHRPE 947
 QY 885 WLHDKYDTTCE-NLRIPPAQPLSFAQPPFLLRGLQKTADFEVATEGARAACAAGQAGVH 943
 DB 948 WVDKADYMPETRLRIPAAEPIYAQPPFFYLNGLRDTSDEFAIEKVRTICSNYTSGLS 1007
 QY 944 AYPGSPFLFEQVGLRRCFLAVCILLVCTFLVCALLLNPNWTAGLIVLVLAMTVEL 1003
 DB 1008 SYNGYFFLFEQYIGLRHWLLLFISVVLACTFLVCVFLNPNWTAGIIVVVLAMTVEL 1067
 QY 1004 FGIMFLGKLSAIPVIVLASVIGIVFTVHVALGELTTQSGSRNLRAAHLEHTFAPVT 1063
 DB 1068 FGMGLIGIKLSAVPVVILIASVIGIVFTVHVALGELTTQSGSRNLRAAHLEHTFAPVT 1127
 QY 1064 DGAISTLGLMLAGSHDFDIYVFFAALTIVTLGLLHGLVLLPVLLSILGPPEVI-- 1121
 DB 1128 DGAIVSTLLGLMLAGSEDFDIYVFFAALTIVTLGLVINGLGLVLLPVLLSFPGPYEVSPA 1187
 QY 1122 ---QWKEPSE-----ILSPP-----APQGG 1139
 DB 1188 NGLNRLPTSPPEPPSVVRPAMPFGHTSHSGSDSDSEYSSQTTVSGLSSELRHVEAQA 1247
 QY 1140 G-----LRWG-----ASSLSQSFAR 1155
 DB 1248 GGAHQVIVEATENPVFAHSTVHVHPSHHPPSNRQPHLDGSLPPGQGGQPRRDP 1307
 QY 1141 -----LRWG-----ASSLSQSFAR 1155
 DB 1308 REGMLPPLXPRRDAFEISTEGHSGPSNRARWGPGRGARSHNPNRNPASTAMGSSVPGYCQ 1367
 QY 1156 VTT-----SMTVAIHPPPLPGAYHP 1176
 DB 1368 ITTVTASAVTVAVHPPPVPGGRNP 1393
 RESULT 6
 US-09-754-032-19
 ; Sequence 19, Application US/09754032
 ; Publication No. US2003014838A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; GOODRICH, LISA V
 ; JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/754,032
 ; FILING DATE: 03-Jan-2001
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/540,406
 ; FILING DATE: 06-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-754-032-19

Query Match      53.4%; Score 3348; DB 10; Length 1447;
Best Local Similarity 49.9%; Pred. No. 7.9e-267;
Matches 672; Conservative 203; Mismatches 285; Indels 186; Gaps 18;

QY 12 PSTVTPARTAAPQILAGSL---KAPLMIRAYFOGLLFSLCGCIQRHCGKVLFLGLLAFGA 68
Db 53 PSYC-DAAFALAQISKGATGRKAPLWRAKFORLLFKLGCYIQKNGKFLVVGLLIFGA 111
QY 69 LALGLRMAITETNLEQLWVEGSRVSOELHYTEKLGEEAAVTSQMLIOTAROBENILT 128
Db 112 FAVGLKAANLETVVEELWVEGSRVSELNYTKQIGEEAFNPQIMIQTPKEEGANVLT 171
QY 129 PEALGLHLQALTASKVQVSLYKSGMDLNKIKYKSGVPLIENGMIEMIEKLPFCVILTP 188
Db 172 TEALLQHLDSALQASRVHVYVYVYRWKLEHLCKYKSGELITETGYMDQIIEYLXPLIITP 231
QY 189 LDCFWEAGAKLOGSAYLPGRPDIQWNLLDPEQLLEELGPF-ASLEGPRELLDKAQQVQAY 247
Db 232 LDCFWEAGAKLOGSAYLPGRPDIQWNLLDPEQLLEELGPF-ASLEGPRELLDKAQQVQAY 291
QY 248 VGRPCLHPDDLHCPSPAHSHSQAPNVAHELSGGCHGFSGHKWQOEELLGLGMARDPQ 307
Db 292 MDRPCLNPADPCPATAPNKNSTKPLDMALVNLGCGHGRKRYMHWOEEELVIGTGVKNST 351
QY 308 GELLREALQSTFLLSPROLYEHRFG-DYQTDHIGWSESEQASTVLAQWQRRFVQLAQEA 366
Db 352 GLVSAHALQTMQLMTPKQWYEHFKGYEVSH-INWNEKAAALAEAWQRTVVEVHQ 410
QY 367 LPNASQIHFASSTLDDILHAFSEVSAARVVGYYLLMLAYACVWMLRWDCAQSGSVG 426
Db 411 VAQNSTQKLSFTTTTLLDDILKSFSDVSVIRVASGYLLMLAYACVWMLRWDCAQSGAVG 470
QY 427 LAGVLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFTEALPG-- 484
Db 471 LAGVLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFSETQNK 530
QY 485 TPLQERMGECQLRTGTSWLTSINNMAAFMAALVPIPALRAFSLQAAIYVGCTTFVAVML 544
Db 531 IPEDRTGECQLRTGASVALTSINVTAFPAALIPALRAFSLQAAVVFVNFAMVLL 590
QY 545 VFPAILSLDLRRHRCORLDVLCFSPSCSAQVITQLPQELGD-----GTVPVGAIAH-- 595
Db 591 IFPAILSMDLRYREDRLDIFCCFTSPCVSRVQVEPQAVTDHNTRYSPPPPYSSH 650
QY 596 -----LTATVQAFTHCEASSQHVITLPPQAHVPPP-----SDPLGSELFSPGSTRD 644
Db 651 AHETQITMQSTVQLRTSYDHPHTHYVYTTABPRSSISQVPTVTDLTSCSPSSTSTRD 710
QY 645 LLGQEEETRQKACSLPCARNLNLAHAFYQFAPLLIQSHAKAIVLFLGALLGLSLYGA 704
Db 711 LLSQFSDS--SLHCLPEPCTKWTLSSEAKEYAFPLKPKAVVVIFFLGLLGVSLYGT 768
QY 705 TLVQDGLHALTDVVRGKHEHAFSAQRYFSLYEVALVTQGGFYAHSQBALFDLHORFS 764
Db 769 TRVRDGLDLTDIVPRETREYDFIAAQKYSFYNNYIVTQKA-DYPNIQHLLYDLHRSFS 827
QY 765 SLKAVLPPPAQAPRTWLYHRYRWLQIQAFADODWASGRITRHSYNGSEEDGNLAYKLL 824
Db 828 NVKYWMLNEKNQLPKMWLHYFRDMLQGLQAFDSDWETKIMPNYKNGSDGGLVAYKLL 887
QY 825 IQTGDAQEPLDPSQLTTRTKLVDRGLIPPELFYMGTLVWVSSDPLGLAASQANFYPPPPPE 884
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RESULT 7

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US-10-421-446-19
; Sequence 19, Application US/10421446
; Publication No. US20030186309A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
;              GOODRICH, LISA V
;              JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
```

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 1447 amino acids

NAME: 14, amino acid
TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE	DESCRIPTION:	SEO ID NO:
19:		

US-10-421-446-19

Query Match	53.4%	Score 3348;	DB 14;	Length 1447;
Best Local Similarity	49.9%	Pred. NO. 7.9e-267;		
Matches 672; Conservative	203;	Mismatches 285;	Indels 186;	Gaps 18;

12	QY	PSYTPPARTAAPOLLAGSL--KAPLMRAYFOGLLPSLGGCQIQRHCGKVLFLGLLAFGA	68
53	DB	PSYC-DAAPFALEQISKSGKATGRKAPLMRAKFORLLFKJGCIYQKNGCKFLVWGLLFGA	111
69	QY	LALGRMAIITETNLEQLWVEGGRSVSOELHYHTEKLGEEAAYTSQMLIQIARQEGENILT	128
112	DB	FAVGLKAANLETVNVEELWVEGGRSVRELNTRYOKIGEEAMFNQPMIQPKBEGANVLT	171
129	QY	PEALGLHLQAALTASKVQVLSYGKSDWLNKICYKSGVPLIENGMIEMWIEKLPFCVILTPT	188
172	DB	TEALLQHLDSALQAASRVHVVMYNRQWLEHLCHYKSGELIETETGYMDQIIEYLYPCLITPT	231
189	QY	LDCFWEKAKLOGGSAYLPGRPDITQWNLDPOLLLEELGPP-ASLEGREGLLDKAAQVGOAY	247
232	DB	LDCFWEKAKLOGSGTAYLLGKPPKRWTFDPDLEELKKINYQVDSWEEMLNKAEBVGHGY	291
248	QY	VGRPCLHPDLDLHCPPSPAPNHHRSQAPNVVAHELSCGCHGFSHKFMHWQBELLLGGMARDPQ	307
292	DB	MDRPCLNPADPCPATAPNKNSTKPLDMALVINGCHGLSKRYMHWQBELIVGTVKVNST	351
308	QY	GELLRABALQSTFLLMSPROLYEHFRG-DYQTHDIGHSEBOASTVLOAWQRRFVOLAQEA	366
352	DB	GKLVSAHALQTMQLMATPKOMYEHFKGYEVYSH-INWNEDKAAALIAEAWQRTYYEVVHQ	410
367	QY	LPENASQOIHAFSSTLDDILHAFSEVSAARVWGYLLMLAYACVWMLRWDCASQGSVG	426
411	DB	VAQNSTQKVLSFTYTTLLDDILKSFSDSVIVRVASGYLLMLAYACLTMLRWDCSKSQNAV	470
427	QY	LAVLLVALAVASGLGICALLGITFNAAATQVLPFLPALGIGVDVDFLLAHAFTALPG--	484
471	DB	LAVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLPALGVGDVDVFLLAHAFTSETQWKR	530
485	QY	TPLOERMGECLORTGTSVWLTSINNMAAFMLAALVPIPALRAPASLOAIVVGCTFVAVML	544
531	DB	IPFEDRTGCKRTGASVALTSISNVTAFFMAALIPIPALRAPASLOAAVVVVFAMVLL	590
545	QY	VFAILLSLDLRRHRCORLDCFCSPSCSAQVIOILPOELGD-----GTVPVGVIAH--	595
591	DB	IFFAILLSMDLYRRDRDLDFCCFTSPCVSERVIOVEPQAYTDHNTREYSPPPYSSHSF	650
596	QY	-----LTATVQAFTHCEASSQHVVTILPPQAHLVPPP-----SDPLGSELFLSPGGSTRD	644
651	DB	AHETQITMQSTVOLRTEYDPHTHYVYTTAEPRSEISVQPVTVITQDLSLCSQSPSTSTRD	710
645	QY	LLGQEEETROKCAKSLPCARWNLAHAFYQFAPLILLOSHAKAIVLVLFGALLGLSLYGA	704
711	DB	LLSQFSDS--SLHCLPEPCTKWTLUSSFAEKHYAPFLPKAKVWVIFLFLGLLGSVLYGT	768
705	QY	TLVODGLALTDVPRGRKEHAFLSLAQRLYFSLYEVALVTQGGFQYAHQSQRALFDLHORFS	764
769	DB	TRVEDGLDLTDIVPRETEYDFIAAQPKYFSYNMYIVTQKA-DYPNIQHLLYDLHRSFS	827
765	QY	SLKAVLPPPPATQAPRTHLYYRNWLQGIQAADFQDNWASGRITRHSYRNGSDEGALAYKLL	824
828	DB	NVKYVMLEENKQLPKPMVLFDRWLQGLQDAFSDSWETGKMLPNPNYKNGSDGVLAYKLL	887

		TYPE: amino acid			
		STRANDEDNESS: single			
		TOPOLOGY: linear			
		MOLECULE TYPE: protein			
		US-08-954-70JA-10			
		Query Match 53.2%; Score 3337; DB 8; Length 1434;			
		Best Local similarity 53.1%; Pred. No. 6.3e-266;			
		Matches 672; Conservative 206; Mismatches 309; Indels 78; Gaps 20;			
QY	3	RSPPREL--PPSYTPARTAAQIIAGSL---	KAPLWLRAYFQGLLSFGCGGIQRHCGK	57	
DB	28	RAAPDRDYLHPSYC-DAAPALEQISKGATGRKAPLWLRAYFQGLLSFGCGGIQRHCGK	86		
QY	58	VFLGGLAFGALGLRMAIETNLEQALWVEGSRVSOELHYTKELGEEAAYTSQMLIQ	117		
DB	87	FLVUGLLIFGAFVGLKAANLETNVLEWVEGSRVSELYNTRQKIGEEAMFNQPMIQ	146		
QY	118	TARQEGENILTPBALGLHQAALTASKVQVSLYCKSWDLNKKIKYKSGVPLIENGMIEMI	177		
DB	147	TPKEEGANVLTTEALLOHLDLSAQASRVHYVYMYNRQWKLHLCYKSGELITETGYMDQII	206		
QY	178	EKLFPVCVILTPCLCFMEGAKLQGSAYLPCRPDIQWNTNLPDEQLLELPGF-ASLEGFRE	236		
DB	207	EYLYPCLLIITPLDCFMEGAKLQGSAYLPCRPDIQWNTNLPDEQLLELPGF-ASLEGFRE	266		
QY	237	LDDKAQGVQAVRCPCLHPDHLCPSPAPNHSRQAPNVAHELSCGCHGSHKPMHWOEE	296		
DB	267	MLNKAIEVGHGYMDRCPCLHPDHLCPSPAPNHSRQAPNVAHELSCGCHGSHKPMHWOEE	326		
QY	297	LLGGWARDPQGLLRALQSTFLMSPROLYEHFRG-DYQTHDIGWSEBQASTVLQAW	355		
DB	327	LIUVGTVKNATGKLVSAHALQWTFQMTPKOMYEHFRGYDVSH-INWEDRAAAILQAW	385		
QY	356	QRFPVLAQBALPENASQQIHAFSTTLDLILHAFSEVSAAARVVGGLMLAYACVTMLR	415		
DB	386	QRTVVEVHQSVAPNSTQKVLPTTTTDDILKSFSDSVIRVASGVYLLMLAYACVTMLR	445		
QY	416	WDCAQSGSVGLAGVLLVALAVASGLICALLGITFNAAATQVLPFLALGIGVDDVFLA	475		
DB	446	WDCSKSQAVGLAGVLLVALAVASGLICALLGITFNAAATQVLPFLALGIGVDDVFLA	505		
QY	476	HAFTEALPG--TPOERMGCLOKRTGTSVVLTSINNMAAFMAALVPALPAPAFSLQAAI	533		
DB	506	HAFSETGONKRIPEDEBTGELKRTGASVALTISINTVAFMAALVPALPAPAFSLQAAV	565		
QY	534	VVGCTFVAVMLVPAILSLDLRRHCRQLDVLCCFSPCSAQVIQIIPQELG-----	586		
DB	566	VVVFNFAMVLLIFPAILSLDLRRHCRQLDVLCCFSPCSAQVIQIIPQELG-----	625		
QY	587	GTVPVGLAH-----LTATVQAFTHCEASSQHVVTILPQAHVLPVP-SDPLGS	633		
DB	626	SPPPPYTSHSAFHETHITMOSITVQLRTEYDPHTVYTTAEPRSEISVQPVTVTDNLSC	685		
QY	634	ELFSPGSTRDLLOEBEETQKAACKSLPCARNLHAFARYQAPLILQSHAKAIVLVLF	693		
DB	686	QSPSTSSRDLDSQFSDS--SLHCLPEPTCKTILSSFAEKHYAPFLKPKAKVWVILLF	743		
QY	694	GALLGLSLYGATLVQDGLALTVDVPRGTKEHAFLSAQLRYSFYVALVTOGGFDYAHSQ	753		
DB	744	LGLLGLSVLYGTTVRDGLDLDIVPRETREYDFIAAQKFKFSFYNMYIVTQKA-DYPNIQ	802		
QY	754	RALFDLHORFSSIKAVLPPPATQAPRTWLHYRNWLOGIOAAFDQDQWASGRITRHSYRNG	813		
DB	803	HLLYDLHKSFSNRYKVMLEENKQLPQWMLHYFRDLQGLQDQAFDSWETGRINPNYKNG	862		
QY	814	SEDGALAYKLLIOTGDAQEPLDPSQLTRKLVREGILPPELFYMGTLVWVSSDPLGLAA	873		
DB	863	SDGVLAUKLVTOGSRDKFIDISLQTKRQLVDADGLINPSAFYIYLTAWNSDPVAYAA	922		
QY	874	SQANFYPPPEWLHDKYDTTGE-NLRIPPAQPLPFAQFPFLRLGLQKTDADFVEAIEGARA	932		
DB	923	SQANIRPHRPEWHDKADYMPETRLRIPAAEPIEYAAQFPFLYNGLRDTSDTFVEAIEKVRV	982		

QY	933	ACAERAGQGVHAYPSGSPFLFWEOYLGLRRCFFLLAVCILLVCTFLVCALLLNPWTAGLI	992		
DB	983	ICNNYTSLSGLSYNGVPFLFWEOYISLRHLLLSISVWLACTFLVCVFLNPWTAGII	1042		
QY	993	VLVLAMTVELFGIMGFLGKLSAIPVVLIVASVIGIVEFTVHVALGFLTTCGRNLRRA	1052		
DB	1043	VNVLAMTVELFGIMGFLGKLSAIPVVLIVASVIGIVEFTVHVALGFLTTCGRNLRRA	1102		
QY	1053	HALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLGLLHGLVLLPVLS	1112		
DB	1103	LALHEWFAPVLDGAVSTLLGVMLAGSEFDFIVRYFFAVALTLVGLVNLGLVLLPVLS	1162		
QY	1113	ILGPPPEVI-----QMYKSPSEILSP-----APQGGGLRWGASSLPSQFARVTS--	1159		
DB	1163	FFGPCPEVPSANGLNRLPTSPS--PPPSVVRFAVPPGHTNNGSDSDSEYSGTTVSGI	1220		
QY	1160	-----MTVAIHPPPLPGAYIHP-APDEPPHSPAA---TSSGNLS	1194		
DB	1221	SEELQYBAQQAGGAPAHQVIVEATENPVFARSTVHVHPDSRHOPLTPROQPHLDGSLT	1280		
QY	1195	SRGPG 1199			
DB	1281	---PG 1282			
RESULT 9					
US-09-754-032-10					
; Sequence 10, Application US/09754032					
; Publication No. US20030148388A1					
; GENERAL INFORMATION:					
; APPLICANT: SCOTT, MATTHEW P					
; GOODRICH, LISA V					
; JOHNSON, RONALD L					
; TITLE OF INVENTION: Patched Genes and their Use					
; NUMBER OF SEQUENCES: 19					
; CORRESPONDENCE ADDRESS:					
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert					
; STREET: Four Embarcadero Center, Suite 3400					
; CITY: San Francisco					
; STATE: CA					
; COUNTRY: US					
; ZIP: 94111					
; COMPUTER READABLE FORM:					
; MEDIUM TYPE: Floppy disk					
; COMPUTER: IBM PC compatible					
; OPERATING SYSTEM: PC-DOS/MS-DOS					
; SOFTWARE: PatentIn Release #1.0, Version #1.30					
; CURRENT APPLICATION DATA:					
; FILING DATE: 03-Jan-2001					
; APPLICATION NUMBER: US/09/754,032					
; CLASSIFICATION: 435					
; PRIOR APPLICATION DATA:					
; APPLICATION NUMBER: US/08/540,406					
; FILING DATE: 06-OCT-1995					
; ATTORNEY/AGENT INFORMATION:					
; NAME: Rowland, Bertram I					
; REGISTRATION NUMBER: 20015					
; REFERENCE/DOCKET NUMBER: a60190-1					
; TELECOMMUNICATION INFORMATION:					
; TELEPHONE: 415-781-1989					
; TELEFAX: 415-398-3249					
; INFORMATION FOR SEQ ID NO: 10:					
; SEQUENCE CHARACTERISTICS:					
; LENGTH: 1434 amino acids					
; TYPE: amino acid					
; TOPOLOGY: linear					
; STRANDEDNESS: single					
; MOLECULE TYPE: protein					
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:					
US-09-754-032-10					
Query Match		53.2%;		Score 3337;	DB 10; Length 1434;

Query Match 53.2%; Score 3337; DB 10; Length 1434;

933 ACAEAGQAVHAYPSGSPFLFWBOYLGLRRCFLAVCILVCTFLVCALLLNPNWTAGLI 992
 983 ICNNYTSLSGSSYPNGYPFLFWBOYISLRHLLSISVLAFLCAVFLNPNWTAGII 1042
 993 VLVAMMTVELFGIMFGFLGKLSAIPVILVASVIGIEFTVHVALGFLTTOGSRNLRAA 1052
 1043 VMVLAAMTVELFGIMFGFLGKLSAIPVILVASVIGIEFTVHVALGFLTTOGSRNLRAA 1102
 1053 HALEHFPAPVTDGAI STLGLMLAGSHDFIYRFFAALTVLTLGLLHGLVLPVLS 1112
 1103 LALEHMFAPVLDGAVSTLLGLVLMAGSEDFIYRFFAALTVLTLGLLHGLVLPVLS 1162
 1113 ILGPPPEVI-----QWYKESPEILSP-----APOGGGLRWGSSSLPOSFARVTTSS-- 1159
 1163 FFGPCPEVSPANGLNRLPTSPSE--PPSVVRFAVPPGHTNNGSDSDSYSQTTVSGI 1220
 1160 -----MTVAIHPPPLPGAYIHP-APDEPPWPSPAA---TSSGNLS 1194
 1221 SEELRQYEAQAGGAPAHQVIVEATENPVFARSTVVPDSRHQPPLTPRQPHLDGSL 1280
 1195 SRGPG 1199
 1281 ---PG 1282

RESULT 9
 US-09-754-032-10
 ; Sequence 10, Application US/09754032
 ; Publication No. US20030148388A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/754,032
 ; FILING DATE: 03-Jan-2001
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/540,406
 ; FILING DATE: 06-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1434 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 ; US-09-754-032-10

MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1296
OTHER INFORMATION: /note= "amino acids encoded by human
nevoid basal cell carcinoma syndrome
(NBCCS) (PATCHED (PTC)) CDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-302-279-60

Query Match 48.6%; Score 3048; DB 14; Length 1296;
Best Local Similarity 49.0%; Pred. No. 4.2e-242;
Matches 610; Conservative 192; Mismatches 261; Indels 182; Gaps 17;

QY 110 YTSQMLTQARQEGENITLALGLHQAALTASKQVSLYKSWDKNKICYKSGVPLIE 169
DB 2 FNQLMLQTPKEGANVLTTEALLQHLDSALQASRVHVMYRNQWKLHLICYKSGELITE 61

QY 170 NGMIEWMIEKLPFCVILTPDCFWEGAKLQGSAYLPGRPDIQWNIIDPQLLEELGPF- 228
DB 62 TGYMDQIIEVLYPLCLITPLDCFWEGAKLQSGTAYLLGKPLRTWTFDLEFLEELKIN 121

QY 229 ASLEGFPELLDKAQGVYGRPCPLHDDLLHCPSPANHHSRQAPNVAHLSGCGHFSH 288
DB 122 YQVDSWEEMLNKAEVGHYMDRCPCLNPAIDPCATAPKNSTKPLDMALVLNGCHGLSR 181

QY 289 KFMHWQBELLLGGWARDPQGBELLRAEALQSTFLMSRQLYEHPRG-DYOTHDIQWSEBQ 347
DB 182 KYMHQBELLVGGIVKNSTKLVSAHALQWFMQMTKQWYEHKGYEYVSH-INNWEDK 240

QY 348 ASTVLAQWRFRVOLAQALPENASQOIHPASSFTLDDILHAFSEVSAARVVGYLMLLA 407
DB 241 AAALIEAQRTYVEVHQSVQAQNSTQVLSFTTTTDDILKFSQVSVIRVASGYLLMLA 300

QY 408 YACVTMLRWDCAQSGVGLAGVLLVALAVASGLGCLALGITNAATTQVLPFLAIGIG 467
DB 301 YACVTMLRWDCSKSQGAVGLAGVLLVALSVAAAGLGLGSLIGISFNAATTQVLPFLAIGV 360

QY 468 VDDVFLAHAFTEALPG--TPQBRMGECIQRCTSVLTSINNMAAPLMAALVPIPALR 525
DB 361 VDDVFLAHAFSEGGQKRPFFEDRTGECLKRTGASVALTSISNVTAFMAALVPIPALR 420

QY 526 AFSLOAAIVVCGTFAVAVMLVFPAILSLDLRRHRCQRLDVLCCFSSPCSAQVIQLPQELG 585
DB 421 AFSLOAAVVVVFNAVLLIFPAIILSMDLYRRERDRLDIFCCFTSPCVSRVIOVQAYT 480

QY 586 D-----GTPVGVIAH-----LTATVQATHCEASQHVVTILPQAHVLPVP-- 627
DB 481 DTHDNTRYSPPPYSSSHSAFHTQITMQSTVQLTEYDPHTHYVYTTAEPREISVQFVT 540

QY 628 --SDPLGSELFSPGSGSTRDLIGQEEETRQAKCKSLPCARNLAFARYOFAPLILLOSHA 685
DB 541 VTQTLSCQSPSTSTRDLISQSDS--SLHCLPEPCTKWTLSFPAKHVAPFLLPKA 598

QY 686 KAVLVFLGALLGLSLGATLVQDGLALTVDVVRGTKEHAFSLAQRLYSFLYVALVTQG 745
DB 599 KVVVIFELGLGLSVLGTTRVRDGLTDIVPRETREYDFIAAQFKYFSFYNNVIYVTK 658

QY 746 GFDYAHQORALFDLHQRFSSLKAVLPPATQAPRTWLHYRNWLOGIQAPDQDQWASRI 805
DB 659 A-DYPNIQHLIYDLHRSFSNKKYVMLENKQLPKWMLHYFRDMLQGLQDAPDSWETGKI 717

QY 806 TRHSYRNGSEGLAYKLLIQTGAQBPDLPSQLTTRKLVDRGLIPPELFYMGLTVMVS 865
DB 718 MPNNYKNGSDGVLAYKLLVGTGRDKPIDISQTLKQRLVDADGIIINPSAFIYILTAWVS 777

QY 866 SDPLGLAASQANFPYPPPEMLHDKYDTTGE-NLRIPPAQPLEFAQFPFLRGLQKTDV 924
DB 778 NDPVYAAASQANIRPHPEWHDKADYMPETRLIPAAEPYEAQFPFLYNGLRDTSDFV 837

QY 925 EAIEGARACAAQAGVAYPSGSPFLFWBQYIQLRRCFLLAVCIILVCTFLVCAILL 984
DB 838 EAIKVRTICSNYTSGLGSSYPNGYPLFWBQYIQLRRHLLIFTSVVLACTFLVCAVFL 897

QY 985 NPWTAGLIVLVLAMMTVELFGIMGFLGKLSAIPVWILVASVGIVGVEFTVHVALGFLTQ 1044
DB 898 NPWTAGIIVVVALMTVLEFGMGLIGKLSAIPVWILVASVGIVGVEFTVHVALFLTAI 957

QY 1045 GSRNLRAHALEHTFAPVTDGAISTLGLMLAGSHDFIVRYFAALTIVTLGLLHGL 1104
DB 958 SDKNRAVALAHMFAPVLDGAVSTLGLVLMAGSEDFIVRYFAVLAAILTILGLVNL 1017

QY 1105 VLLPVLISILGPPPEV----- 1120
DB 1018 VLLPVLISFGPPEVSPANGLNRLPTSPPEPPSVVRPAMPPOGTHSGSDSSSEYSSQ 1077

QY 1121 -----IQMY----- 1130
DB 1078 TTVSGLSEELRHYEAQAGGAPAHQVIVEATENPVFAHSTVVPESRHHPPSPKQPHL 1137

QY 1131 LS---PPAQG-----GGL-----RWG----- 1144
DB 1138 DSGSLPFGQGGQPRDRPRKGLMPLLYRPRRDAFEISTEGHSGPSNRARMGPRGARSHN 1197

QY 1145 -----ASSLPOSPARVTT-----SMTVAIHPPPLPGAYIHP 1176
DB 1198 PRNPTSTAMGSSVPGYCPITTTVASAVTVAVHPPVPVPGGRNP 1242

RESULT 12

US-08-954-701A-4
; Sequence 4, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-954-701A-4

Query Match 35.6%; Score 2235; DB 8; Length 1311;

Best Local Similarity 39.9%; Pred. No. 7.1e-175;

Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;

QY 18 ARTAAPQILAGSL---KAPLWLRAYFQGLLFLSLGCGIQRHCGKVLFLGLLAFGALGLR 74

Db 41 AALASELEKNGTEGGRTSLWIRAWLQQLFILGCFQDGAGKVLVAILVLSTFCVGLK 100
QY 75 MAIETNLEQLWVEVSRVQELHYHTEKLGEBEAAVTSQMLIQIARQEGENILTPALGL 134
Db 101 SAQIHTRVLDQLWQEGGRLEAEKXYTAQALGEADSDSTHOLVIQTAKDPDVSLLHPGALLE 160
QY 135 HLQAALTASKVQVSLYKGSNDLANKICYKSGVPLIEN-GMIEMIEKLPFCVILTPDLDCF 193
Db 161 HLKVHVAATRVTHMYDIEWRLKDLVLCYSPSPDPFEGVHHIESIIDNVIPCAIITPLDCFW 220
QY 194 EGAKLOGGS--AYLPG-RPDIQWNTLDPQELLEBLG-----PFASLEGRELLDKAQVG 244
Db 221 EGSKLLGPDYPIYVPHLKHKLQWHLNPLEVVEEVKLFQFPPLSTIEAY--MKRAGIT 277
QY 245 QAVVGRPLCHDDLHCPSPAPNHHISROAPNVAHELSGGCHGFHSHKFMHWOBEILLGGMAR 304
Db 278 SAYMKKPCLDPTDPHCPATAPNKKSGHIPDVAEELSHGCGYFAAAVYHWPQELIVGATR 337
QY 305 DPQELLRAEALOSTFLMSPROLIYEHFRGDYQTHDIGWSEEOASTVLQAWORREVQLAQ 364
Db 338 NTSALRKARXLQTVQVMGEREMEYEMADHYKHQIGMNOEKAAAVLDAWQRKPAEVR 397
QY 365 EALPE---NASQIHAFFSSTLDDILHAFSEVSAARVVGGLMLLAYACVYTLRW-DCAQ 420
Db 398 KITTSQSVSSAYSFPSTSTLNDILGKFSEVSLKNIILGYMFMILYVAVTLIQWRDP 457
QY 421 SQSGVGLAGVLLVALAVASGIGLCALLGTFNAATQVLPFLALGIGVDVDFLLAHAFTE 480
Db 458 SQAGVGIAGVLLSITVAAGLGFALLGIPFNASSTQIVPFLALGIGVQDMFLTHTYE 517
QY 481 ALPCTPLQERWGECLQRTGTSVVLTSINMAAFIMAAVLPALRAFSLQAAIIVVGCTFV 540
Db 518 QAGDVPREETGLVLRKSGSUSVLLASCNWFALAAALLPIPAFRVFCLOQAIIILLFNLG 577
QY 541 AVMLVFPAILSLDLRRHRCORLDVLCF--SSPCSQVQIQLPQELGDDGVTVPGIAHLTA 598
Db 578 SILLVFPAMISLDRRSARADLLCLMPESP-----LPK-----KIP----- 617
QY 599 TVQAFTHCEASSQHVVTILPQOHLVPPSPDPLGSELFPSSGSTRDLGQEEETROKAA 658
Db 618 -----BRAKTRKNDKTHRIDTTRQPLDPDV-----SENVTKTCC 651
QY 659 KSLPCARWNLAHFARYQFAPLLQSHAKAIVLVLFGALLGLSLYGATLVODGLALTDVVP 718
Db 652 LVSLLTKW-----AKQYAPFIRMPAVKVTSMALTAIVLTSTVWGATKVKDGLDIDVP 706
QY 719 RGTKEHAFSLAQLRYFSLYEVALVTOGGDFDYAHQSQRALFDLHORFSLKAVLPPPATQAP 778
Db 707 ENTDEHEFLSRQEKYFGFYNNYAVTQGNFEYPTNQKLLIYEHQDFVRIPIIKNDNGGLT 766
QY 779 RTWLHYRNWLOGIQAAFDQDMSAGRITRHSY-RNGSEDGALAYKLLIQTGAQEPDLDFS 837
Db 767 KFWLSLFRDMLLDQVAFDKVEASGCITQBYWCKNASDEGILAYKLMVQTHVDNPDKS 826
QY 838 QLIT-RKLDVREGLIPELFWMGITVWVSSDPLGLAASQANFYPPPEWLHDXVDITGEN 896
Db 827 LITAGHRLVDKGIINPKAFNYLSAWATNDALAYGASQGNLKPQORWHTSPEDV---H 883
QY 897 LRTPPAQPLFAFPFLLRGLQKTADPVEAIEGARAAACAEAGQAGVHAYPSGSPFFLFWEQ 956
Db 884 LEIKKSPLYITQLPFLVSLGSDTXSIKTLIRSVRDLCLAYEAKPLNFPSPGIPFLFWEQ 943
QY 957 YLGRRCFLLAVCILLVCTFLVCAILLNPNWTHAGLIVLVLAMTVELFGIMFGIKLSA 1016
Db 944 YLYLRTSLLLALACAAAFVIAVNVLLNNAWAAVLTALATATVLQLLGMVALLGVKLSA 1003
QY 1017 IPVVLVAVSGIGVEFTVHVAFGLTFTQGSRNLRRAAHLEHTAPVTDGAISTLLGLML 1076
Db 1004 MPAVLLVLAIGRWHFVHLICLGFVTSIGCKRRRASLATESVLAPOVHGAALAAALASML 1063
QY 1077 AGSHFDFIVRYFFAALTNLGLLHGLVLLPVLSTLGGPPPEVIQMYKESPBILSPAP 1136

Db 1064 AASECGFVARLFLRLLLDIVFLGLIDGLLFFPIVLSILGPAEVRPI--EHPERLSTPSP 1121
QY 1137 Q-----GGLRWGAASSLPSQSFARVTTSMT 1161
Db 1122 KCSPIHPRKSSSSGGGDKSSRTSKSAPRPCAPSLTTIT 1160
RESULT 13
US-09-754-032-4
; Sequence 4, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-754-032-4
Query Match 35.6%; Score 2235; DB 10; Length 1311;
Best Local Similarity 39.9%; Pred. No. 7.1e-175;
Matches 470; Conservative 213; Mismatches 402; Indels 94; Gaps 19;
QY 18 ARTAAPQIIAGSL---KAPLWLRAYTQGLLFSLGGCIQRHCGKVLFLGLLAFGALALGLR 74
Db 41 AALALSELEKNGTEGGRTSLWIRAWLQQLFILGCFQDGAGKVLVAILVLSTFCVGLK 100
QY 75 MAIETNLEQLWVEVSRVQELHYHTEKLGEBEAAVTSQMLIQIARQEGENILTPALGL 134
Db 101 SAQIHTRVLDQLWQEGGRLEAEKXYTAQALGEADSDSTHOLVIQTAKDPDVSLLHPGALLE 160
QY 135 HLQAALTASKVQVSLYKGSNDLANKICYKSGVPLIEN-GMIEMIEKLPFCVILTPDLDCF 193
Db 161 HLKVHVAATRVTHMYDIEWRLKDLVLCYSPSPDPFEGVHHIESIIDNVIPCAIITPLDCFW 220
QY 194 EGAKLOGGS--AYLPG-RPDIQWNTLDPQELLEBLG-----PFASLEGRELLDKAQVG 244
Db 221 EGSKLLGPDYPIYVPHLKHKLQWHLNPLEVVEEVKLFQFPPLSTIEAY--MKRAGIT 277

Db	944	IFWEQYMTLRSSLAMILLACVLLAALVLV - SULLSVWA	VLTLSVLASQAIFGAMTLL	1002
Qy	1011	GIKLSAIPVVLINASVGIGVEFTHVALGFLTTQGRNLR	AAHALEHTFAPVTDGAISTL	1070
Db	1003	GIKLSAIPAVILLISVGMMLCFNVLSLGFMTSVGNR	QVOLSQMSLGPLVHGMLTSG	1062
Qy	1071	LGLMLAGSHDFIVRYFFAALTVLTLGLLHGLVLLP	VLLSTILGPPPEVIQYKSPRI	1130
Db	1063	VAVFMLSTSPPEFVIRHFCVWLLLVLCVGCACNSL	LVFPILLMSVGPBEALVPL - EHPDR	1120
Qy	1131	LSPAP	1136	
Db	1121	ISTPSP	1126	

Search completed: June 14, 2005, 16:27:58
Job time : 185 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 08:01:47 ; Search time 177 Seconds
(without alignments)

Title: US-09-990-046A-2

Perfect score:

Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSSRGGPATG 1203

Scoring table: OLIGO

Scoring scale: CHSO
Gapop 60.0 , Gapext 60.0

Searched: 1714042 seqs, 383979560 residues

Word size :

Total number of hits satisfying chosen parameters: 1714042

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/pdata/2/pubpaa/us07_PUBCOMB.pcp.*
- 2: /cgn2_6/pdata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/pdata/2/pubpaa/us06_NEW_PUB.pcp.*
- 4: /cgn2_6/pdata/2/pubpaa/us06_PUBCOMB.pcp.*
- 5: /cgn2_6/pdata/2/pubpaa/us07_NEW_PUB.pcp.*
- 6: /cgn2_6/pdata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
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- 8: /cgn2_6/pdata/2/pubpaa/us08_PUBCOMB.pcp.*
- 9: /cgn2_6/pdata/2/pubpaa/us09A_PUBCOMB.pcp.*
- 10: /cgn2_6/pdata/2/pubpaa/us09B_PUBCOMB.pcp.*
- 11: /cgn2_6/pdata/2/pubpaa/us09C_PUBCOMB.pcp.*
- 12: /cgn2_6/pdata/2/pubpaa/us09_NEW_PUB.pcp.*
- 13: /cgn2_6/pdata/2/pubpaa/us10A_PUBCOMB.pcp.*
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- 18: /cgn2_6/pdata/2/pubpaa/us10F_NEW_PUB.pcp.*
- 19: /cgn2_6/pdata/2/pubpaa/us11A_PUBCOMB.pcp.*
- 20: /cgn2_6/pdata/2/pubpaa/us11_NEW_PUB.pcp.*
- 21: /cgn2_6/pdata/2/pubpaa/us16_NEW_PUB.pcp.*
- 22: /cgn2_6/pdata/2/pubpaa/us60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			Description	
	Score	Match	Length	ID	
1	1203	100.0	1203	9	US-09-990-046-2
2	900	74.8	1203	9	US-09-909-280A-2
3	94	7.8	1182	9	US-09-990-046-7
4	15	1.2	1296	14	US-10-302-279-60
5	15	1.2	1434	8	US-08-954-701A-10
6	15	1.2	1434	10	US-09-754-032-10
7	15	1.2	1434	14	US-10-421-446-10
8	15	1.2	1447	8	US-08-954-701A-19
9	15	1.2	1447	9	US-09-898-533-5
10	15	1.2	1447	10	US-09-754-032-19
11	15	1.2	1447	14	US-10-421-446-19
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					Sequence 2, Appli
					Sequence 7, Appli
					Sequence 60, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 10, Appl
					Sequence 5, Appli
					Sequence 19, Appl
					Sequence 19, Appl

85 8 0.7 321 14 US-10-029-386-31960 Sequence 31960, A
86 8 0.7 332 15 US-10-282-122A-69254 Sequence 69254, A
87 8 0.7 379 15 US-10-369-493-623 Sequence 623, App
88 8 0.7 379 17 US-10-732-923-4165 Sequence 4165, App
89 8 0.7 385 15 US-10-282-122A-51177 Sequence 51177, A
90 8 0.7 406 15 US-10-424-599-171492 Sequence 171492, A
91 8 0.7 409 15 US-10-282-122A-68715 Sequence 68715, A
92 8 0.7 416 16 US-10-437-963-102663 Sequence 102663, A
93 8 0.7 445 14 US-10-239-316-35 Sequence 35, Appl
94 8 0.7 456 14 US-10-239-316-34 Sequence 34, Appl
95 8 0.7 479 16 US-10-788-792-186 Sequence 186, App
96 8 0.7 489 15 US-10-424-599-190164 Sequence 190164, A
97 8 0.7 531 10 US-09-899-642-2 Sequence 2, Appli
98 8 0.7 531 16 US-10-767-701-46169 Sequence 46169, A
99 8 0.7 531 17 US-10-732-923-24086 Sequence 24086, A
100 8 0.7 548 16 US-10-473-127-1454 Sequence 1454, Ap

ALIGNMENTS

RESULT 1

US-09-990-046-2
; Sequence 2, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990,046
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-046-2

Query Match 100.0%; Score 1203; DB 9; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTRSPPLELPSPYTPPARTAAPQILAGSLKAPLWLRAYFQGLFSLGCGIQRHCGKVL 60
Db 1 MTRSPPLELPSPYTPPARTAAPQILAGSLKAPLWLRAYFQGLFSLGCGIQRHCGKVL 60
Qy 61 LGLAFAGALGLRMAIETNLEQLWVEVGSRSQELHYTKELGEBAAVTSQMLIQAR 120
Db 61 LGLAFAGALGLRMAIETNLEQLWVEVGSRSQELHYTKELGEBAAVTSQMLIQAR 120
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Db 121 QEGENILTPALGHLQALTASKQVSLYCKSWDLNKICYKGVPLIENGMIEMWLEKL 180
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Db 181 PPCVILPLDFCWEGAKLQGSAYLPGRPDIQWNLDPQELBELGPFASLEGFRELDDK 240
Qy 241 AQVQAVVGRPCPLHDDDLHCPSPAPNHHRSQAPNVAHELSCGCHGFSGHKFMHWQBEILLG 300
Db 241 AQVQAVVGRPCPLHDDDLHCPSPAPNHHRSQAPNVAHELSCGCHGFSGHKFMHWQBEILLG 300
Qy 301 GMARDPQELLRAELQSTFLMSPROLYEHFRGDYQTHDIGWSEEOASTVLAQWRFFV 360
Db 301 GMARDPQELLRAELQSTFLMSPROLYEHFRGDYQTHDIGWSEEOASTVLAQWRFFV 360
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Db 361 QLAQEALPENASQOIHAFFSSTLDDIILHAFSEVSAARVVGGLMLLAYACVYMLRWDCAQ 420

Qy 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLFALGIGVDVFLLAHAFT 480
Db 421 SQGSVGLAGVLLVALAVASGLGICALLGITFNAATTQVLPFLFALGIGVDVFLLAHAFT 480
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Db 481 ALPGTPLQRMGECIQRCTGTSVVLTISINNAAPLMAALVPIPALRAFSLOAIIVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHCORLDVLCFSSPCSAQVIQILPOELGDTGVPVGAHTATV 600
Db 541 AVMLVFPAILSLDLRRHCORLDVLCFSSPCSAQVIQILPOELGDTGVPVGAHTATV 600
Qy 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDLGSELSPGSTRDLGQSEETRQKAACKS 660
Db 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDLGSELSPGSTRDLGQSEETRQKAACKS 660
Qy 661 LPCARWNLAFHAFARYQFAPLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTVDVPRG 720
Db 661 LPCARWNLAFHAFARYQFAPLLQSHAKAIVLVLFGALLGLSLYGATLVQDGLALTVDVPRG 720
Qy 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPPATQAPRT 780
Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSORALFDLHORFSSLKAVLPPPATQAPRT 780
Qy 781 WLHYRNWLQGIOAAFDQDQWASGRITRHSYRNGSEDGALAYKLLIOTGDAQEPDLSOLT 840
Db 781 WLHYRNWLQGIOAAFDQDQWASGRITRHSYRNGSEDGALAYKLLIOTGDAQEPDLSOLT 840
Qy 841 TRKLDVREGLIPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLDVREGLIPELFYMGITVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQPFLLRGLQKTADFVEAIEGARACACAGQVHAYPSSGPFLEWQYIGL 960
Db 901 PAQPLEFAQPFLLRGLQKTADFVEAIEGARACACAGQVHAYPSSGPFLEWQYIGL 960
Qy 961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVLAMTVELFGIMFGLIGIKLSAIPV 1020
Db 961 RRCFLAVCILVCTFLVCALLLNPNWTAGLIVLVLAMTVELFGIMFGLIGIKLSAIPV 1020
Qy 1021 ILVASVGIGVEFTVHVVALGFLTQGSRNLRRAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
Db 1021 ILVASVGIGVEFTVHVVALGFLTQGSRNLRRAHALEHTFAPVTDGAISTLLGLMLAGSH 1080
Qy 1081 FDIIVYFFAALTVLTLGLLHGLVLLPVLLSTILGPPPEVIQMYKESPEILSPAPQGG 1140
Db 1081 FDIIVYFFAALTVLTLGLLHGLVLLPVLLSTILGPPPEVIQMYKESPEILSPAPQGG 1140
Qy 1141 LRWGASSLPQSPARVTTSMTVAIHPPLPGAYIHPAPDEPPMSPAATSSGNLSRGP 1200
Db 1141 LRWGASSLPQSPARVTTSMTVAIHPPLPGAYIHPAPDEPPMSPAATSSGNLSRGP 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 2

US-09-909-280A-2
; Sequence 2, Application US/09909280A
; Patent No. US20020160375A1
; GENERAL INFORMATION:
; APPLICANT: Buncroft, David A.
; TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
; TITLE OF INVENTION: THERETO
; FILE REFERENCE: CIBT-P02-050
; CURRENT APPLICATION NUMBER: US/09/909,280A
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/207,857
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 60/067,940
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1203
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-990-280A-2

Query Match 74.8%; Score 900; DB 9; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MTRSPPIRELPSTTPPARTAAPQILAGSLKAPILWLRAYFQGLLFSIGCGIQRHCGKVL	60
Db	1	MTRSPPIRELPSTTPPARTAAPQILAGSLKAPILWLRAYFQGLLFSIGCGIQRHCGKVL	60
Qy	61	LGLAFGALALGLRWAIETNLEOLWVEGSRVSOELHYTKELGEEAAVTSQWLIQTAR	120
Db	61	LGLAFGALALGLRWAIETNLEOLWVEGSRVSOELHYTKELGEEAAVTSQWLIQTAR	120
Qy	121	QEGENILTPALGLHLQAALTASKVQVSLYCKSWDLNKKI CYKSGVPLIENGMIEMIEKL	180
Db	121	QEGENILTPALGLHLQAALTASKVQVSLYCKSWDLNKKI CYKSGVPLIENGMIEMIEKL	180
Qy	181	PPCVILTPDCFWGAKLQGSAYLPGRPDIQWNTNLPDPELLEBGFASLEGFRELDDK	240
Db	181	PPCVILTPDCFWGAKLQGSAYLPGRPDIQWNTNLPDPELLEBGFASLEGFRELDDK	240
Qy	241	AQVQAVGVRPCLHPDDLHCPPSPAPNHHSRQAPNVAHELGGCHGFSKEMHWOELLG	300
Db	241	AQVQAVGVRPCLHPDDLHCPPSPAPNHHSRQAPNVAHELGGCHGFSKEMHWOELLG	300
Qy	301	GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLOAWQRRFV	360
Db	301	GMARDPOGELLRAEALQSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLOAWQRRFV	360
Qy	361	QLAQEALPENASQOIHAFFSTTDLIDILHAFSEVSAARVGGYLLMLAYCVTMLRWDCAQ	420
Db	361	QLAQEALPENASQOIHAFFSTTDLIDILHAFSEVSAARVGGYLLMLAYCVTMLRWDCAQ	420
Qy	421	SQGSVGLAGVLLVALAVASGLGICGALGIFTNAAATQVLPFLALGIGVDVDFLLAHAFTE	480
Db	421	SQGSVGLAGVLLVALAVASGLGICGALGIFTNAAATQVLPFLALGIGVDVDFLLAHAFTE	480
Qy	481	ALPCTPLQERMGECLQRTGTSVLTSINNMAAFMAALVPIPALRAFSLQAALVVGCTFV	540
Db	481	ALPCTPLQERMGECLQRTGTSVLTSINNMAAFMAALVPIPALRAFSLQAALVVGCTFV	540
Qy	541	AVMLVFPAILSLDLRRRHQRDLVLCFSSPCSAQVIQILPQELGDCGTVPVGHIAHLTATV	600
Db	541	AVMLVFPAILSLDLRRRHQRDLVLCFSSPCSAQVIQILPQELGDCGTVPVGHIAHLTATV	600
Qy	601	QAFTHCEASSQHVVTILPQAHVLPSPDPLGSELFPGGSTRDLLQOESETRQKAACKS	660
Db	601	QAFTHCEASSQHVVTILPQAHVLPSPDPLGSELFPGGSTRDLLQOESETRQKAACKS	660
Qy	661	LPCARNWLAHFARYQAPLLOSHAKAI VLVLFCALLGLSLYGATLVQDGLALTDVVPRG	720
Db	661	LPCARNWLAHFARYQAPLLOSHAKAI VLVLFCALLGLSLYGATLVQDGLALTDVVPRG	720
Qy	721	TKEHAFSLAQRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSLSKAVLPFPATQAPRT	780
Db	721	TKEHAFSLAQRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSLSKAVLPFPATQAPRT	780
Qy	781	WLHYRNWLOGIQAAFQDQWASGRITRHSYRNSEDCALAYKLLIQTGDAQEPLDFSQLT	840
Db	781	WLHYRNWLOGIQAAFQDQWASGRITRHSYRNSEDCALAYKLLIQTGDAQEPLDFSQLT	840
Qy	841	TRKLVDRGLIPPELFTWGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP	900
Db	841	TRKLVDRGLIPPELFTWGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP	900
Qy	901	PAQPLEFAQFPFLRLGLQKTADFEALLEGARAAACAEAGQAGVHAYPSGSPFLFWEQYVGL	960
Db	901	PAQPLEFAQFPFLRLGLQKTADFEALLEGARAAACAEAGQAGVHAYPSGSPFLFWEQYVGL	960

Db	901	PAQPLEFAQFPFLRLGLQKTADFEALLEGARAAACAEAGQAGVHAYPSGSPFLFWEQYVGL	960
Qy	961	RRCFLLAVCTLLVCTFLVCAALLLNPNWTAGLIVLVLAMTVELFGIMGPIGKLSAIPVV	1020
Db	961	RRCFLLAVCTLLVCTFLVCAALLLNPNWTAGLIVLVLAMTVELFGIMGPIGKLSAIPVV	1020
Qy	1021	ILVASVGIGVEFTVHVVALGFLTTQGSRNRAAAHLEHTFAPVTDGAIETSLGLMLAGSH	1080
Db	1021	ILVASVGIGVEFTVHVVALGFLTTQGSRNRAAAHLEHTFAPVTDGAIETSLGLMLAGSH	1080
Qy	1081	FDIVRYFFAALTVLTLGLLHGLVLLPVLLSLGPPPEVIQMYKESPEILSPAPQGGG	1140
Db	1081	FDIVRYFFAALTVLTLGLLHGLVLLPVLLSLGPPPEVIQMYKESPEILSPAPQGGG	1140
Qy	1141	LRWGASSLPQSPARVTTMTVAIHPPPLPGAIYHPADPPMSPAAATSSGNLSRGGPG	1200
Db	1141	LRWGASSLPQSPARVTTMTVAIHPPPLPGAIYHPADPPMSPAAATSSGNLSRGGPG	1200
Qy	1201	ATG 1203	
Db	1201	ATG 1203	

RESULT 3
US-09-990-046-7
; Sequence 7, Application US/09990046
; Patent No. US20020156245A1
; GENERAL INFORMATION:
; APPLICANT: de Sauvage, Frederic
; APPLICANT: Carpenter, David A.
; TITLE OF INVENTION: Patched-2
; FILE REFERENCE: P1405R1
; CURRENT APPLICATION NUMBER: US/09/990, 046
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293,505
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 7
; LENGTH: 1182
; TYPE: PRN
; ORGANISM: Mus musculus
US-09-990-046-7

Query Match 7.8%; Score 94; DB 9; Length 1182;
Best Local Similarity 100.0%; Pred. No. 7.3e-76;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	693	FGALLGLSLYGATLVQDGLALTDVPRGTKEHAFSLAQRYFSLYEVALVTQGGFDYAH	752
Db	693	FGALLGLSLYGATLVQDGLALTDVPRGTKEHAFSLAQRYFSLYEVALVTQGGFDYAH	752
Qy	753	QRALFDLHQRFSLSKAVLPFPATQAPRTWLHYR 786	
Db	753	QRALFDLHQRFSLSKAVLPFPATQAPRTWLHYR 786	

RESULT 4
US-10-302-279-60
; Sequence 60, Application US/10302279
; Publication No. US20030171566A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael Carlton
; Hahn, Heidi Eye
; Wickling, Carol
; Christiansen, Jeffrey
; Zaphiropoulos, Peter G.
; Gailani, Mae R.
; Shanley, Susan Mary
; Chidambaram, Abirami
; Vorechovsky, Igor
; Holmberg-Lindstrom, Erika
; TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene
; NUMBER OF SEQUENCES: 84

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;;
;; ZIP: 94111-3834
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/302,279
;; FILING DATE: 22-NO. US20030171566A1-2002
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/857,636
;; FILING DATE: 16-MAY-1997
;; APPLICATION NUMBER: US 60/017,906
;; FILING DATE: 17-MAY-1996
;; APPLICATION NUMBER: AU P00011
;; FILING DATE: 21-MAY-1996
;; APPLICATION NUMBER: AU P00363
;; FILING DATE: 07-JUN-1996
;; APPLICATION NUMBER: US 60/019,765
;; FILING DATE: 14-JUN-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hyman, Laurence J.
;; REGISTRATION NUMBER: 35, 551
;; REFERENCE/DOCKET NUMBER: 015280-278200US
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;;
;; INFORMATION FOR SEQ ID NO: 60:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1296 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..1296
;; OTHER INFORMATION: /note="amino acids encoded by human
;; nevoid basal cell carcinoma syndrome
;; (NBCCS) (PATCHED (PTC)) cDNA"
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-10-302-279-60

Query Match 1.2%; Score 15; DB 14; Length 1296;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 344 FNAATTQVLPLALG 358

RESULT 5
US-08-954-701A-10
; Sequence 10, Application US/08954701A
; Publication No. US20030032085A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston

;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII(text)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/954,701A
;; FILING DATE: 20-OCT-1997
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Vincent, Matthew P.
;; REGISTRATION NUMBER: 36709
;; REFERENCE/DOCKET NUMBER: SUV-003.08
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-832-1000
;; TELEFAX: 617-832-7000
;;
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1434 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
US-08-954-701A-10

Query Match 1.2%; Score 15; DB 8; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

RESULT 6
US-09-754-032-10
; Sequence 10, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1434 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-754-032-10

Query Match 1.2%; Score 15; DB 10; Length 1434;
 Best Local Similarity 100.0%; Pred. No. 0.00061;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 Db 481 FNAATTQVLPLALG 495

RESULT 7
 US-10-421-446-10
 ; Sequence 10, Application US/10421446
 ; Publication No. US20030186309A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/421,446
 ; FILING DATE: 22-Apr-2003
 ; CLASSIFICATION: <Unknown>

; APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/724,631
 ; FILING DATE: 28-No. US20030186309A1-2000
 ; APPLICATION NUMBER: US/08/656,055
 ; FILING DATE: 1996-05-31
 ; APPLICATION NUMBER: 08/540,406
 ; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: a60190-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1434 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-10-421-446-10

Query Match 1.2%; Score 15; DB 14; Length 1434;
 Best Local Similarity 100.0%; Pred. No. 0.00061;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 Db 481 FNAATTQVLPLALG 495

RESULT 8
 US-08-954-701A-19
 ; Sequence 19, Application US/08954701A
 ; Publication No. US20030032085A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SCOTT, MATHEW P
 ; APPLICANT: GOODRICH, LISA V
 ; APPLICANT: JOHNSON, RONALD L
 ; TITLE OF INVENTION: Patched Genes and their Use
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley, Hoag & Eliot
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII(text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/954,701A
 ; FILING DATE: 20-OCT-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36709
 ; REFERENCE/DOCKET NUMBER: SUV-003.08
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1447 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; MOLECULE TYPE: protein
 ; MOLECULE TYPE: protein

; Query Match 1.2%; Score 15; DB 8; Length 1447;
 ; Best Local Similarity 100.0%; Pred. No. 0.00061;
 ; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 Db 495 FNAATTQVLPLALG 509

RESULT 9
 US-09-898-533-5
 ; Sequence 5, Application US/09898533
 ; Patent No. US20020106656A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gemmill, Robert M.
 ; APPLICANT: Drabkin, Harry A.
 ; TITLE OF INVENTION: TRCS, A GENE RELATED TO THE HEDGEHOG RECEPTOR,
 ; TITLE OF INVENTION: PATCHED
 ; FILE REFERENCE: 93445-00004
 ; CURRENT APPLICATION NUMBER: US/09/898,533
 ; CURRENT FILING DATE: 2001-07-02
 ; PRIOR APPLICATION NUMBER: US/09/268,140
 ; PRIOR FILING DATE: 2000-03-12
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 5

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; LENGTH: 1447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-898-533-5

Query Match          1.2%; Score 15; DB 9; Length 1447;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 10
US-09-754-032-19
; Sequence 19, Application US/09754032
; Publication No. US20030148388A1
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,032
; FILING DATE: 03-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,406
; FILING DATE: 06-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-754-032-19

Query Match          1.2%; Score 15; DB 10; Length 1447;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 11
US-10-421-446-19
; Sequence 19, Application US/10421446
; Publication No. US20030186309A1

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; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; GOODRICH, LISA V
; JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/421,446
; FILING DATE: 22-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,631
; FILING DATE: 28-No. US20030186309A1-2000
; APPLICATION NUMBER: US/08/656,055
; FILING DATE: 1996-05-31
; APPLICATION NUMBER: 08/540,406
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: a60190-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-421-446-19

Query Match          1.2%; Score 15; DB 14; Length 1447;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 495 FNAATTQVLPLALG 509

RESULT 12
US-10-369-493-5410
; Sequence 5410, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374

```

; SEQ ID NO 5410
; LENGTH: 714
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5410

Query Match 0.8%; Score 11; DB 15; Length 714;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 VGIGVEFTVHV 1036
Db 660 VGIGVEFTVHV 670
|||||

RESULT 13

US-10-369-493-5464
; Sequence 5464, Application US/10369493
; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 5464

; LENGTH: 1405

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-5464

Query Match 0.8%; Score 11; DB 15; Length 1405;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1026 VGIGVEFTVHV 1036
Db 1242 VGIGVEFTVHV 1252
|||||

RESULT 14

US-10-239-316-17

; Sequence 17, Application US/10239316

; Publication No. US20030125253A1

; GENERAL INFORMATION:

; APPLICANT: TANIYAMA, Yoshio

; APPLICANT: KITA, Shunbun

; APPLICANT: SATOMI, Tomoko Komiya

; TITLE OF INVENTION: No. US20030125253A1el Protein, Process for Producing The Same And

; FILE REFERENCE: 2703USOP

; CURRENT APPLICATION NUMBER: US/10/239,316

; CURRENT FILING DATE: 2002-09-19

; PRIOR APPLICATION NUMBER: PCT/JP01/02279

; PRIOR FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: JP2000-088595

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 59

; SEQ ID NO 17

; LENGTH: 1087

; TYPE: PRT

; ORGANISM: Human

US-10-239-316-17

Query Match 0.8%; Score 10; DB 14; Length 1087;
Best Local Similarity 100.0%; Pred. No. 17;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1106 LLPVLJSILG 1115
Db 903 LLPVLJSILG 912
|||||

RESULT 15

US-10-621-758A-2

; Sequence 2, Application US/10621758A

; Publication No. US20040093629A1

; GENERAL INFORMATION:

; APPLICANT: Altmann, Scott W

; APPLICANT: Wang, Luquan

; APPLICANT: Graziano, Michael

; APPLICANT: Murgolo, Nick

; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF

; FILE REFERENCE: JB01603-K-US

; CURRENT APPLICATION NUMBER: US/10/621,758A

; CURRENT FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: 60/397,442

; PRIOR FILING DATE: 2002-07-19

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1331

; TYPE: PRT

; ORGANISM: Rattus sp.

US-10-621-758A-2

Query Match 0.8%; Score 10; DB 15; Length 1331;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TLGLLHGLV 1105
Db 1248 TLGLLHGLV 1257
|||||

RESULT 16

US-10-663-208A-2

; Sequence 2, Application US/10663208A

; Publication No. US20040132058A1

; GENERAL INFORMATION:

; APPLICANT: Altmann, Scott W

; APPLICANT: Wang, Luquan

; APPLICANT: Graziano, Michael

; APPLICANT: Murgolo, Nick

; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF

; FILE REFERENCE: JB01603K2 US

; CURRENT APPLICATION NUMBER: US/10/663,208A

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: 60/397,442

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 10/621,758

; PRIOR FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: 10/646,301

; PRIOR FILING DATE: 2003-08-22

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 1331

; TYPE: PRT

; ORGANISM: Rattus sp.

US-10-663-208A-2

Query Match 0.8%; Score 10; DB 16; Length 1331;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TLGLLHGLV 1105
Db 1248 TLGLLHGLV 1257
|||||

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RESULT 17
US-10-646-301A-2
; Sequence 2, Application US/10646301A
; Publication No. US20040137467A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: J01603-K1-US
; CURRENT APPLICATION NUMBER: US/10/646,301A
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/621,758
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1331
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-646-301A-2

Query Match          0.8%; Score 10; DB 16; Length 1331;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
    |||||
Db 1248 TLLGLLHGLV 1257

RESULT 18
US-10-736-769-2
; Sequence 2, Application US/10736769
; Publication No. US20040161838A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: J01603-K3-US
; CURRENT APPLICATION NUMBER: US/10/736,769
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/621,758
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 10/646,301
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 10/663,208
; PRIOR FILING DATE: 2003-09-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1331
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-736-769-2

Query Match          0.8%; Score 10; DB 16; Length 1331;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
    |||||
Db 1248 TLLGLLHGLV 1257

```

```

RESULT 19
US-10-239-316-9
; Sequence 9, Application US/10239316
; Publication No. US20030125253A1
; GENERAL INFORMATION:
; APPLICANT: TANIYAMA, Yoshio
; APPLICANT: KITA, Shunbun
; APPLICANT: SATOMI, Tomoko Komiya
; TITLE OF INVENTION: No. US20030125253A1 Protein, Process for Producing The Same An
; FILE REFERENCE: 2703USOP
; CURRENT APPLICATION NUMBER: US/10/239,316
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: PCT/JP01/02279
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-088595
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 59
; SEQ ID NO 9
; LENGTH: 1332
; TYPE: PRT
; ORGANISM: Human
US-10-239-316-9

Query Match          0.8%; Score 10; DB 14; Length 1332;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
    |||||
Db 1247 TLLGLLHGLV 1256

RESULT 20
US-10-621-758A-4
; Sequence 4, Application US/10621758A
; Publication No. US20040093629A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: J01603-K-US
; CURRENT APPLICATION NUMBER: US/10/621,758A
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-758A-4

Query Match          0.8%; Score 10; DB 15; Length 1332;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
    |||||
Db 1247 TLLGLLHGLV 1256

RESULT 21
US-10-663-208A-4
; Sequence 4, Application US/10663208A
; Publication No. US20040132058A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael

```

; APPLICANT: Murgolo, Nick
 ; TITLE OF INVENTION: NPC11 (NPC3) AND METHODS OF USE THEREOF
 ; FILE REFERENCE: JB01603K2 US
 ; CURRENT APPLICATION NUMBER: US/10/663,208A
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: 60/397,442
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 10/621,758
 ; PRIOR FILING DATE: 2003-07-17
 ; PRIOR APPLICATION NUMBER: 10/646,301
 ; PRIOR FILING DATE: 2003-08-22
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 1332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-663-208A-4

Query Match 0.8%; Score 10; DB 16; Length 1332;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
 |||||
 Db 1247 TLLGLLHGLV 1256

RESULT 22
 US-10-646-301A-4
 ; Sequence 4, Application US/10646301A
 ; Publication No. US20040137467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altmann, Scott W
 ; APPLICANT: Wang, Luquan
 ; APPLICANT: Murgolo, Nick
 ; TITLE OF INVENTION: NPC11 (NPC3) AND METHODS OF USE THEREOF
 ; FILE REFERENCE: JB01603-K1-US
 ; CURRENT APPLICATION NUMBER: US/10/646,301A
 ; CURRENT FILING DATE: 2003-08-22
 ; PRIOR APPLICATION NUMBER: 60/397,442
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 10/621,758
 ; PRIOR FILING DATE: 2003-07-17
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 1332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-646-301A-4

Query Match 0.8%; Score 10; DB 16; Length 1332;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
 |||||
 Db 1247 TLLGLLHGLV 1256

RESULT 23
 US-10-736-769-4
 ; Sequence 4, Application US/10736769
 ; Publication No. US20040161838A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altmann, Scott W
 ; APPLICANT: Wang, Luquan
 ; APPLICANT: Murgolo, Nick
 ; TITLE OF INVENTION: NPC11 (NPC3) AND METHODS OF USE THEREOF
 ; FILE REFERENCE: JB01603-K3-US

; CURRENT APPLICATION NUMBER: US/10/736,769
 ; CURRENT FILING DATE: 2003-12-16
 ; PRIOR APPLICATION NUMBER: 60/397,442
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 10/621,758
 ; PRIOR FILING DATE: 2003-07-17
 ; PRIOR APPLICATION NUMBER: 10/646,301
 ; PRIOR FILING DATE: 2003-08-22
 ; PRIOR APPLICATION NUMBER: 10/663,208
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 1332
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-736-769-4

Query Match 0.8%; Score 10; DB 16; Length 1332;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
 |||||
 Db 1247 TLLGLLHGLV 1256

RESULT 24
 US-10-621-758A-12
 ; Sequence 12, Application US/10621758A
 ; Publication No. US20040093629A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altmann, Scott W
 ; APPLICANT: Wang, Luquan
 ; APPLICANT: Murgolo, Nick
 ; TITLE OF INVENTION: NPC11 (NPC3) AND METHODS OF USE THEREOF
 ; FILE REFERENCE: JB01603-K-US
 ; CURRENT APPLICATION NUMBER: US/10/621,758A
 ; CURRENT FILING DATE: 2003-07-17
 ; PRIOR APPLICATION NUMBER: 60/397,442
 ; PRIOR FILING DATE: 2002-07-19
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 12
 ; LENGTH: 1333
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-10-621-758A-12

Query Match 0.8%; Score 10; DB 15; Length 1333;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
 |||||
 Db 1248 TLLGLLHGLV 1257

RESULT 25
 US-10-663-208A-12
 ; Sequence 12, Application US/10663208A
 ; Publication No. US20040132058A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Altmann, Scott W
 ; APPLICANT: Wang, Luquan
 ; APPLICANT: Murgolo, Nick
 ; TITLE OF INVENTION: NPC11 (NPC3) AND METHODS OF USE THEREOF
 ; FILE REFERENCE: JB01603K2 US
 ; CURRENT APPLICATION NUMBER: US/10/663,208A
 ; CURRENT FILING DATE: 2003-09-16
 ; PRIOR APPLICATION NUMBER: 60/397,442

; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/621,758
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 10/646,301
; PRIOR FILING DATE: 2003-08-22
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1333
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-663-208A-12

Query Match 0.8%; Score 10; DB 16; Length 1333;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TLLGLLHGLV 1105
Db 1248 TLLGLLHGLV 1257

RESULT 26
US-10-646-301A-12
; Sequence 12, Application US/10646301A
; Publication No. US20040137467A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: JB01603-K1-US
; CURRENT APPLICATION NUMBER: US/10/646,301A
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/621,758
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1333
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-646-301A-12

Query Match 0.8%; Score 10; DB 16; Length 1333;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TLLGLLHGLV 1105
Db 1248 TLLGLLHGLV 1257

RESULT 27
US-10-736-769-12
; Sequence 12, Application US/10736769
; Publication No. US20040161838A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: JB01603-K3-US
; CURRENT APPLICATION NUMBER: US/10/736,769
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/621,758
; PRIOR FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: 10/646,301
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 10/663,208
; PRIOR FILING DATE: 2003-09-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1333
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-736-769-12

Query Match 0.8%; Score 10; DB 16; Length 1333;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TLLGLLHGLV 1105
Db 1248 TLLGLLHGLV 1257

RESULT 28
US-10-621-758A-44
; Sequence 44, Application US/10621758A
; Publication No. US20040093629A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: JB01603-K-US
; CURRENT APPLICATION NUMBER: US/10/621,758A
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 1359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-621-758A-44

Query Match 0.8%; Score 10; DB 15; Length 1359;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TLLGLLHGLV 1105
Db 1274 TLLGLLHGLV 1283

RESULT 29
US-10-663-208A-44
; Sequence 44, Application US/10663208A
; Publication No. US20040132058A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC1L1 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: JB01603K2-US
; CURRENT APPLICATION NUMBER: US/10/663,208A
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/621,758
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 10/646,301
; PRIOR FILING DATE: 2003-08-22
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 1359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-663-208A-44

Query Match 0.8%; Score 10; DB 16; Length 1359;
Best Local Similarity 100.0%; Pred.No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
| | | | | | | | | |
Db 1274 TLLGLLHGLV 1283

RESULT 30
US-10-646-301A-44
; Sequence 44, Application US/10646301A
; Publication No. US20040137467A1
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W
; APPLICANT: Wang, Luquan
; APPLICANT: Graziano, Michael
; APPLICANT: Murgolo, Nick
; TITLE OF INVENTION: NPC111 (NPC3) AND METHODS OF USE THEREOF
; FILE REFERENCE: JBO1603-K1-US
; CURRENT APPLICATION NUMBER: US/10/646,301A
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/397,442
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/621,758
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 1359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-646-301A-44

Query Match 0.8%; Score 10; DB 16; Length 1359;
Best Local Similarity 100.0%; Pred.No. 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
| | | | | | | | | |
Db 1274 TLLGLLHGLV 1283

Search completed: June 16, 2005, 08:12:47
Job time : 181 secs

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OM protein - protein search, using sw model

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(without alignments)

2673.981 Million cell updates/sec

Title: US-09-990-046A-2

Perfect score: 1203

Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSGNLSRRGPGPATG 1203

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Searched: 2105692 seqs, 386760381 residues

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4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1203	100.0	1203	2	AAY43261 Human pat
2	1203	100.0	1203	5	AAY19829 Human pat
3	1203	100.0	1203	6	ABG74104 Human pat
4	900	74.8	1203	2	AAY28444 Human pat
5	888	73.8	1203	3	AAY92703 Human pat
6	839	69.7	1146	3	AAY92225 Human pat
7	497	41.3	529	2	AAY82586 Human pat
8	94	7.8	1182	5	AAY19831 Human pat
9	43	3.6	46	2	AAY82587 Human pat
10	32	2.7	119	4	AAY01960 Human pat
11	15	1.2	608	7	ADD46676 Rat Prote
12	15	1.2	1296	2	AAY47157 Nevoid ba
13	15	1.2	1434	2	AAY94380 Mouse pat
14	15	1.2	1434	2	AAY52199 Mouse pat
15	15	1.2	1434	2	AAY72968 Mouse pat
16	15	1.2	1434	4	AAB67159 Murine pa
17	15	1.2	1434	5	AAG79572 Mouse pat
18	15	1.2	1434	7	ABU62271 Mouse pat
19	15	1.2	1434	7	ADH64215 Murine pt
20	15	1.2	1434	7	ADH62722 Mouse pat
21	15	1.2	1434	8	ADH48980 Mouse pat
22	15	1.2	1447	2	AAY75375 Human pat
23	15	1.2	1447	2	AAY52200 Human pat
24	15	1.2	1447	2	AAY72969 Human pat
25	15	1.2	1447	4	AAB67163 Human pat

26	15	1.2	1447	5	AAE19830	Aae19830 Human pat
27	15	1.2	1447	5	ABJ10931	Abj10931 TRC8 rela
28	15	1.2	1447	5	AAG79571	Aag79571 Human pat
29	15	1.2	1447	7	ABU62275	Abu62275 Human pat
30	15	1.2	1447	7	ADD46678	Add46678 Human pro
31	15	1.2	1447	7	ADH62731	Adh62731 Human pat
32	15	1.2	1447	7	ADH62731	Adh62731 Human pat
33	15	1.2	1447	8	ADH48989	Adh48989 Human pat
34	11	0.9	714	8	ADN22757	Adn22757 Bacterial
35	11	0.9	1405	8	ADN22811	Adn22811 Bacterial
36	10	0.8	269	3	AAB43088	Aab43088 Human ORF
37	10	0.8	314	4	ABG25311	Abg25311 Novel hum
38	10	0.8	532	4	ABG25312	Abg25312 Novel hum
39	10	0.8	1087	4	AAG65640	Aag65640 SSD-contra
40	10	0.8	1331	8	ADJ27295	Adj27295 Rat NPC1L
41	10	0.8	1332	4	AAM79169	Aam79169 Human pro
42	10	0.8	1332	4	AAG56538	Aag56538 SSD-contra
43	10	0.8	1332	8	ADJ27297	Adj27297 Human NPC
44	10	0.8	1333	8	ADJ27305	Adj27305 Mouse NPC
45	10	0.8	1344	4	ABG22693	Abg22693 Novel hum
46	10	0.8	1359	4	AAM79168	Aam79168 Human pro
47	10	0.8	1359	8	ADJ27337	Adj27337 Human NPC
48	10	0.8	1392	4	AAG56544	Aag56544 SSD-contra
49	10	0.8	1561	5	ADH48884	Adh48884 NOV70 pro
50	9	0.7	11	2	AAR94377	Aar94377 Patched p
51	9	0.7	11	2	AAR94377	Aar94377 Patched p
52	9	0.7	11	4	AAB67160	Aab67160 Patched p
53	9	0.7	11	7	ABU62272	Abu62272 Patched g
54	9	0.7	11	7	ADH62723	Adh62723 N-termina
55	9	0.7	11	7	ADH62723	Adh62723 N-termina
56	9	0.7	11	8	ADH48981	Adh48981 Patched g
57	9	0.7	115	2	AAR94384	Aar94384 Mosquito
58	9	0.7	115	2	AAR52198	Aar52198 Anopheles
59	9	0.7	115	2	AAR72973	Aar72973 Anopheles
60	9	0.7	115	4	AAB67158	Aab67158 Mosquito
61	9	0.7	115	5	AAG79575	Aag79575 Mosquito
62	9	0.7	115	7	ABU62270	Abu62270 African m
63	9	0.7	115	7	ADH62720	Adh62720 Mosquito
64	9	0.7	115	7	ADH62720	Adh62720 Mosquito
65	9	0.7	115	8	ADH48978	Adh48978 Mosquito
66	9	0.7	209	2	AAY59784	Aay59784 Human nor
67	9	0.7	329	3	AAG39735	Aag39735 Arabidops
68	9	0.7	354	3	AAG39734	Aag39734 Arabidops
69	9	0.7	435	3	AAG39733	Aag39733 Arabidops
70	9	0.7	730	4	ABB71879	Abb71879 Drosophil
71	9	0.7	1285	2	AAR72972	Aar72972 Drosophil
72	9	0.7	1285	4	AAB67157	Aab67157 Fruit fly
73	9	0.7	1285	5	AAG79574	Aag79574 Drosophil
74	9	0.7	1285	7	ABU62150	Abu62150 Fruit fly
75	9	0.7	1285	7	ADH62718	Adh62718 Fly patch
76	9	0.7	1285	7	ADH62718	Adh62718 Fly patch
77	9	0.7	1285	8	ADH48976	Adh48976 Drosophil
78	9	0.7	1286	4	ABH59092	Abh59092 Drosophil
79	9	0.7	1286	5	ABJ10929	Abj10929 TRC8 rela
80	9	0.7	1299	2	AAR86304	Aar86304 Drosophil
81	9	0.7	1299	4	AAE05389	Aae05389 Human pat
82	9	0.7	1299	4	AAB85751	Aab85751 Hedgehog
83	9	0.7	1299	4	ABH31232	Abh31232 A consens
84	9	0.7	1299	5	ABH79150	Abh79150 Patched p
85	9	0.7	1299	6	ADA26289	Ada26289 Hedgehog-
86	9	0.7	1299	7	ADD25309	Add25309 Hedgehog-
87	9	0.7	1299	7	ABW00878	Abw00878 Drosophil
88	9	0.7	1299	7	ABW01685	Abw01685 Drosophil
89	9	0.7	1299	7	ADH61129	Adh61129 Drosophil
90	9	0.7	1299	7	ADH54692	Adh54692 Drosophil
91	9	0.7	1311	2	AAS52197	Aas52197 Precis co
92	9	0.7	1311	2	AAR72971	Aar72971 Precis co
93	9	0.7	1311	4	AAH67156	Aah67156 Butterfly
94	9	0.7	1311	5	AAG79573	Aag79573 Butterfly
95	9	0.7	1311	7	ABU62149	Abu62149 Peacock b
96	9	0.7	1311	7	ADH48974	Adh48974 Butterfly
97	9	0.7	1311	7	ADH62716	Adh62716 Butterfly
98	9	0.7	1311	8	ADH48974	Adh48974 Butterfly

99 9 0.7 1711 8 ADN46550 Adn46550 Thermococ
100 8 0.7 23 4 ABB76816 Abb76816 Artificia

ALIGNMENTS

RESULT 1
AA43261 ID AA43261 standard; protein; 1203 AA.
XX AC AA43261;
XX 19-JAN-2000 (first entry)
XX Human patched-2 protein sequence.
XX Patched-2; ptch-2; human; signalling molecule; hedgehog cascade; stroke;
XX cell proliferation; cell differentiation; testicular cancer; gut disease;
XX degenerative disorder; nervous system disorder; Parkinson's disease;
XX memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;
XX Huntington's disease; drug addiction; bone disease; skin disease; ulcer;
XX infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;
XX
OS Homo sapiens.
XX
XX WO953058-A1.
XX 21-OCT-1999.
XX 02-APR-1999; 99WO-US007417.
XX 15-APR-1998; 98US-00060939.
XX (GETH) GENENTECH INC.
XX De Sauvage FJ, Carpenter DA;
XX WPI; 1999-620428/53.
XX N-PSDB; AAZ31717.
XX
XX New isolated human patched-2 gene, used to develop products for treating,
XX e.g. cancer and Alzheimer's disease.
XX
XX Claim 14; Fig 1; 124pp; English.
XX
XX This sequence represents the human patched-2 (ptch-2) protein of the
XX invention. The patched-2 polypeptides are signalling molecules,
XX specifically for signalling and mediator molecules in the hedgehog (hh)
XX cascade which are involved in cell proliferation and differentiation.
XX They can be used for the treatment of disorders which are mediated at
XX least in part by Hh, especially Dhh, e.g. testicular cancer. They can
XX also be used for treating degenerative disorders of the nervous system,
XX e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou
XX Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug
XX addiction. Patched-2 agonists can be used to treat gut diseases, bone
XX diseases, skin diseases, diseases of the testis (including infertility),
XX ulcers, lung diseases, diseases of the pancreas, diabetes, and
XX osteoporosis. Antagonists or agonists of patched-2 may be used for
XX treating disorders or creating a desirable physiological condition
XX effected by blocking Hh signalling, especially Dhh signalling, e.g.
XX contraception or infertility treatment. The products can also be used for
XX detection, diagnosis, drug screening and production of transgenic animals
XX
XX Sequence 1203 AA;

Query Match 100.0%; Score 1203; DB 2; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTRSPPRLRPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCGKVL 60
|||||

Db 1 MTRSPPRLRPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLPSLGGCIQRHCGKVL 60
Qy 61 LGLLAFGALALGLRMAIIETNLEQLWVEVSGRSVQSELHYTKKELGEEAAVYTSQMLIQ 120
|||||
Db 61 LGLLAFGALALGLRMAIIETNLEQLWVEVSGRSVQSELHYTKKELGEEAAVYTSQMLIQ 120
Qy 121 QEGENILTPREALGLHLQAAALTASKVQVSLYKGSWDNLNKICYKSGVPLIENGMIEMWIEKL 180
|||||
Db 121 QEGENILTPREALGLHLQAAALTASKVQVSLYKGSWDNLNKICYKSGVPLIENGMIEMWIEKL 180
Qy 181 FPCVILTPDLCFWEKALQGGSAIYLPGRPDIOQTNLDPEQLLEELGEPFASLEGFRELLDK 240
|||||
Db 181 FPCVILTPDLCFWEKALQGGSAIYLPGRPDIOQTNLDPEQLLEELGEPFASLEGFRELLDK 240
Qy 241 AQVQAYVGRPCLLHPDDLHCPPSAPNHSRQAPNVAHELSGGCHGFSHKFMHWQEBLLLG 300
|||||
Db 241 AQVQAYVGRPCLLHPDDLHCPPSAPNHSRQAPNVAHELSGGCHGFSHKFMHWQEBLLLG 300
Qy 301 GWARDPQGLLRABALQSTFLLMSPROLYEHFRGDYQTHDIGWSEQAQSTVLQAWQRRFV 360
|||||
Db 301 GWARDPQGLLRABALQSTFLLMSPROLYEHFRGDYQTHDIGWSEQAQSTVLQAWQRRFV 360
Qy 361 QLAQEAALPENASQOIHAFSSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
|||||
Db 361 QLAQEAALPENASQOIHAFSSTTLDLILHAFSEVSAARVVGYYLLMLAYACVTMLRWDCAQ 420
Qy 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFT 480
|||||
Db 421 SQSGVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIGVDDVFLLAHAFT 480
Qy 481 ALPGTFLQERMGECLQRTGTSVVLTISINNAAPFLMAALVPIPALRAFSLOAAVVGCTFV 540
|||||
Db 481 ALPGTFLQERMGECLQRTGTSVVLTISINNAAPFLMAALVPIPALRAFSLOAAVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIQILPQELGIGTVPVGAHLTATV 600
|||||
Db 541 AVMLVFPAILSLDLRRRHQRDLVLCFSSPSCSAQVIQILPQELGIGTVPVGAHLTATV 600
Qy 601 QAFTHCEASSQHVVTILPQAHVLPVPPSLGSELSPGSGSTRDLGQEBETTRQKAACKS 660
|||||
Db 601 QAFTHCEASSQHVVTILPQAHVLPVPPSLGSELSPGSGSTRDLGQEBETTRQKAACKS 660
Qy 661 LPCARWNLAFARYQFAPILLOSHAKAIVLVLPFALLGLSLYCATIVQDGLALTVDVVRG 720
|||||
Db 661 LPCARWNLAFARYQFAPILLOSHAKAIVLVLPFALLGLSLYCATIVQDGLALTVDVVRG 720
Qy 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSLSKAVLPPPATQAPRT 780
|||||
Db 721 TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHSQRALFDLHQRFSLSKAVLPPPATQAPRT 780
Qy 781 WLHYRNWLOGIQAAFDQDWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEBLDFSOLT 840
|||||
Db 781 WLHYRNWLOGIQAAFDQDWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEBLDFSOLT 840
Qy 841 TRKLVNREGILPELFWMLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
|||||
Db 841 TRKLVNREGILPELFWMLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQPPFLRLGLQKTADFEVEALEGARAACAAGQAGVHAYPSGSPFLFWEQYIGL 960
|||||
Db 901 PAQPLEFAQPPFLRLGLQKTADFEVEALEGARAACAAGQAGVHAYPSGSPFLFWEQYIGL 960
Qy 961 RRCFLLAVCTLLVCTFLVCAALLLNPNWAGLIIVLIVAMTVELFGIMFGIGIKLSAIPV 1020
|||||
Db 961 RRCFLLAVCTLLVCTFLVCAALLLNPNWAGLIIVLIVAMTVELFGIMFGIGIKLSAIPV 1020
Qy 1021 ILVASYGIVGEFTVHVVALGELTTQGSRNRAAHLRHTFAPVTDGAI STLGLLMLAGSH 1080
|||||
Db 1021 ILVASYGIVGEFTVHVVALGELTTQGSRNRAAHLRHTFAPVTDGAI STLGLLMLAGSH 1080
Qy 1081 FDIIVRYFFAALTATLTLGLLHGLVLLPVLLSLTILGPPPEVIOMYKESPEILSPAPQGG 1140
|||||
Db 1081 FDIIVRYFFAALTATLTLGLLHGLVLLPVLLSLTILGPPPEVIOMYKESPEILSPAPQGG 1140

Qy 1141 LRWASSLPQSFARVTTMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
Db 1141 LRWASSLPQSFARVTTMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 2
AAE19829 :
ID AAE19829 standard; protein; 1203 AA.
AC AAE19829;
DT 18-JUN-2002 (first entry)
XX Human patched-2 (Ptch-2) protein.
DE Human; patched-2; Ptch-2; cell proliferation; differentiation; therapy;
KW cytosolic; testicular cancer; hedgehog protein signalling.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Domain 57..76
FT /label= TM1
FT /note= "Transmembrane domain"
FT 394..414
FT /label= TM2
FT /note= "Transmembrane domain"
FT 427..449
FT /label= TM3
FT /note= "Transmembrane domain"
FT 458..477
FT /label= TM4
FT /note= "Transmembrane domain"
FT 502..524
FT /label= TM5
FT /note= "Transmembrane domain"
FT 532..553
FT /label= TM6
FT /note= "Transmembrane domain"
FT 687..705
FT /label= TM7
FT /note= "Transmembrane domain"
FT 964..984
FT /label= TM8
FT /note= "Transmembrane domain"
FT 988..1010
FT /label= TM9
FT /note= "Transmembrane domain"
FT 1014..1033
FT /label= TM10
FT /note= "Transmembrane domain"
FT 1058..1077
FT /label= TM11
FT /note= "Transmembrane domain"
FT 1091..1114
FT /label= TM12
FT /note= "Transmembrane domain"

PN US6348575-B1.
XX
PD 19-FEB-2002.
XX
PF 15-APR-1999; 99US-00293505.
XX
PR 15-APR-1998; 98US-0081884P.
XX
PA (GETH) GENENTECH INC.

PI De Sauvage F, Carpenter DA;
XX WPI; 2002-215260/27.
DR N-PSDB; AAD31576.
XX Native human patched-2 polypeptide for treating disorders caused by
PT Hedgehog protein signaling such as testicular cancer, and for screening
PT cDNA libraries.
XX
PS Example 1; Fig 1; 82pp; English.
XX
CC The invention relates to an isolated sequence comprising a native human
CC patched-2 (Ptch-2) polypeptide. The invention also relates to signalling
CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
CC cell proliferation and differentiation. The isolated sequence is useful
CC for the treatment of disorders which are linked to hedgehog, especially
CC desert hedgehog expression, such as testicular cancer. It may also be
CC used as a hybridisation probe in a cDNA library to isolate Ptch-2 or its
CC homologues, and to diagnose whether a disorder is driven by Ptch-2 or
CC hedgehog protein signalling. The present sequence is human patched-2
CC (Ptch-2) protein
XX
SQ Sequence 1203 AA;
Query Match 100.0%; Score 1203; DB 5; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVL 60
Db 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGKVL 60
Qy 61 LGLLAFGALALGLRMALIIETNLQMLVEGSRVSYQELHYTKLGEAAVTSQMLIQTAR 120
Db 61 LGLLAFGALALGLRMALIIETNLQMLVEGSRVSYQELHYTKLGEAAVTSQMLIQTAR 120
Qy 121 QEGENILTPREALGLHLQAALTASKVQVSLYKGSWDLNKKICKYGVPLIENGMIEMIEKL 180
Db 121 QEGENILTPREALGLHLQAALTASKVQVSLYKGSWDLNKKICKYGVPLIENGMIEMIEKL 180
Qy 181 FPCVILTPDLDFWEGAKLOGGSAYLPGRPDIQWNLDPDPEQLLELPFASLEGFRELDDK 240
Db 181 FPCVILTPDLDFWEGAKLOGGSAYLPGRPDIQWNLDPDPEQLLELPFASLEGFRELDDK 240
Qy 241 AQVGQAVGRPCPLHPDDLHCPSPAPNHHSRQAPNVAHELSGGCHGSHKFMHWOELLG 300
Db 241 AQVGQAVGRPCPLHPDDLHCPSPAPNHHSRQAPNVAHELSGGCHGSHKFMHWOELLG 300
Qy 301 GMARDPQGLLRALAEALQSTFLMSPRQLYEHFRGDYQTHDIGWSEBQASTVLQAWQRRFV 360
Db 301 GMARDPQGLLRALAEALQSTFLMSPRQLYEHFRGDYQTHDIGWSEBQASTVLQAWQRRFV 360
Qy 361 QLAQALPENASQOIHAFFSSTLDDILHAFSEVSAARVGGYLLMLAYACVTMLRWDCAQ 420
Db 361 QLAQALPENASQOIHAFFSSTLDDILHAFSEVSAARVGGYLLMLAYACVTMLRWDCAQ 420
Qy 421 SOGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIVDDVFLLAHAFTE 480
Db 421 SOGSVGLAGVLLVALAVASGLGICALLGITFNAAATQVLPFLALGIVDDVFLLAHAFTE 480
Qy 481 ALPGTFLQERMGECLQRTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
Db 481 ALPGTFLQERMGECLQRTGTSVVLTSINNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
Qy 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPSCAQVIQILPQELGDTVPVGAHLTATV 600
Db 541 AVMLVFPAILSLDLRRHRCORLDVLCFSSPSCAQVIQILPQELGDTVPVGAHLTATV 600
Qy 601 QAFTHCEASSQHVVTILPQAHILVPPSPDLGSELSFGSSTRDLLGQEEETKQKACKS 660
Db 601 QAFTHCEASSQHVVTILPQAHILVPPSPDLGSELSFGSSTRDLLGQEEETKQKACKS 660
Qy 661 LPCARNLAFARYQFAPLLQLSHAKAIVLVLFALLGLSLYGATLVQDGLALTVDVVRPG 720

Db	661	LPARMNLAPARYQFAPLPLQLQSHAKAIVLVLFQALLGLSLGYATLVQDGLATDVVPRG	720
Qy	721	TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSQRALFDLHQRFSSLKAVLPFPATQAPRT	780
Db	721	TKEHAFLSAQLRYFSLYEVALVTQGGFDYAHQSQRALFDLHQRFSSLKAVLPFPATQAPRT	780
Qy	781	WLHYRWNLOGIOAFAPODQWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPLDFSOLT	840
Db	781	WLHYRWNLOGIOAFAPODQWASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPLDFSOLT	840
Qy	841	TRKLVDEGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP	900
Db	841	TRKLVDEGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIP	900
Qy	901	PAQPLEFAQPFLLRGLQKTAADVEALEGARAAACAEAGQAGVHAYPSGSPFLFWEQYIQL	960
Db	901	PAQPLEFAQPFLLRGLQKTAADVEALEGARAAACAEAGQAGVHAYPSGSPFLFWEQYIQL	960
Qy	961	RRCPELLAVCILLVCTFLVCAILLNPNWTAGLIVLVAMMTVELFGIMFGIKLSAIPVV	1020
Db	961	RRCPELLAVCILLVCTFLVCAILLNPNWTAGLIVLVAMMTVELFGIMFGIKLSAIPVV	1020
Qy	1021	ILVASVGIVGEFTHVVALGFLTTQGSRLRAAHALEHTAPVTDGATSTLLGLMLAGSH	1080
Db	1021	ILVASVGIVGEFTHVVALGFLTTQGSRLRAAHALEHTAPVTDGATSTLLGLMLAGSH	1080
Qy	1081	FDFTVRYFFAALTVTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG	1140
Db	1081	FDFTVRYFFAALTVTLGLLHGLVLLPVLLSILGPPPEVIQMYKESPEILSPAPQGGG	1140
Qy	1141	LRWGASSLPQSFAFVTTSMVTVAIHPPPPLPGAYIHPAPDEPPWSPAATSGNLSRRGPG	1200
Db	1141	LRWGASSLPQSFAFVTTSMVTVAIHPPPPLPGAYIHPAPDEPPWSPAATSGNLSRRGPG	1200
Qy	1201	ATG 1203	
Db	1201	ATG 1203	
XX	RESULT 3		
ID	ABG74104		
XX	AC		
XX	ABG74104 standard; protein; 1203 AA.		
XX	ABG74104;		
DT	02-APR-2003 (first entry)		
XX	Human patched-2 protein.		
DE	Human; patched-2; Dhh signaling; proliferation; differentiation;		
XX	chromosome 1p33-34; male contraceptive; infertility; spermatogenesis;		
KW	basal cell carcinoma; neurodegenerative disorder; memory deficit;		
KW	Alzheimer's disease; Parkinson's disease; Lou Gehrig's disease;		
KW	Huntington's disease; schizophrenia; stroke; drug addiction; gut disease;		
KW	bone disease; skin disease; testicular disease; ulcer; lung disease;		
KW	pancreatic disease; diabetes; osteoporosis; desert hedgehog.		
OS	Homo sapiens.		
XX	US2002156245-A1.		
PN	24-OCT-2002.		
PD	20-NOV-2001; 2001US-00990046.		
XX	15-APR-1998; 98US-0081884P.		
PR	15-APR-1999; 99US-00293505.		
XX	(GETH) GENENTECH INC.		
PA	De Sauvage FJ, Carpenter DA;		
XX			

DR	WPI: 2003-182650/18.
DR	N-PSDB; ABX15919.
XX	
PT	New nucleic acid, useful for manufacturing a medicament for diagnosing or
PT	treating a disorder that is modulated by Desert hedgehog (Dhh) signaling
PT	e.g., testicular cancer.
XX	
XX	Claim 14; Fig 1; 85pp; English.
XX	
CC	The invention relates to a new isolated nucleic acid encoding a
CC	polypeptide having patched-2 biological activity, comprises DNA having at
CC	least 9% sequence identity with a DNA molecule or its complement
CC	encoding: (a) a human patched-2 polypeptide comprising the sequence
CC	ABG74104; or (b) the same mature polypeptide encoded by the cDNA (ATCC
CC	Deposit No. 209778 designation). Also included are a vector comprising
CC	the nucleic acid, a host cell transformed with the vector, a process for
CC	producing patched-2 polypeptides, an isolated native sequence of human
CC	patched-2 polypeptide, a chimeric molecule comprising the vertebrate
CC	patched-2 polypeptide and a heterologous (aa) sequence, an antagonist of
CC	patched-2 (that blocks, prevents, inhibits and/or neutralises the Desert
CC	hedgehog (Dhh) function in the Dhh signalling pathway), an agonist of
CC	patched-2 that stimulates or enhances the normal functioning of patched-2
CC	in the Dhh signalling pathway, screening for ant/agonists of patched-2
CC	and diagnosing to determine whether a particular disorder is modulated
CC	The nucleic acid is useful for manufacturing a medicament for diagnosing
CC	or treating a disorder that is modulated by Dhh signalling e.g. tumour,
CC	basal cell carcinoma, neurodegenerative disorders, memory deficit,
CC	Alzheimer's disease, Parkinson's disease, Lou Gehrig's disease,
CC	Huntington's disease, schizophrenia, stroke, drug addiction, gut
CC	diseases, bone diseases, skin diseases, testicular diseases, ulcers, lung
CC	diseases, pancreatic diseases, diabetes, osteoporosis and infertility.
CC	Patched-2 may also be used to develop male contraceptives. The gene for
CC	Patched-2 is located on human chromosome 1p33-34. The present sequence
CC	represents human patched-2 protein
XX	
SQ	Sequence 1203 AA;
	Query Match 100.0%; Score 1203; DB 6; Length 1203;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MTRSPRLRELPPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSLGCGIQRHCGKLVF 60
Db	1 MTRSPRLRELPPSYTPPARTAAPQILAGSLKAPLMLRAYFQGLLFSLGCGIQRHCGKLVF 60
Qy	61 LGLLAFGALGALGRMAIIETNLEQLMVVEGSRVSOELHYTKYKELGEEAAYTSQMLIQATAR 120
Db	61 LGLLAFGALGALGRMAIIETNLEQLMVVEGSRVSOELHYTKYKELGEEAAYTSQMLIQATAR 120
Qy	121 OEGENTILTPREALGHLQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIETWMEKL 180
Db	121 OEGENTILTPREALGHLQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIETWMEKL 180
Qy	181 FPCVILTPLDCFWEGAKLOGGSAYLPGRPDIQWNTLNDPEQLLELGPFPASLEGFRELLDK 240
Db	181 FPCVILTPLDCFWEGAKLOGGSAYLPGRPDIQWNTLNDPEQLLELGPFPASLEGFRELLDK 240
Qy	241 AQVQYAVYGRPCLLHPDDLHCPSPAPNHHSRQAPNVAHELSGGCHGSHKFMHWQEBLLLG 300
Db	241 AQVQYAVYGRPCLLHPDDLHCPSPAPNHHSRQAPNVAHELSGGCHGSHKFMHWQEBLLLG 300
Qy	301 GMARDPQELLRAELAQSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLQAWORRFV 360
Db	301 GMARDPQELLRAELAQSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLQAWORRFV 360
Qy	361 QLAQEALPENASQOIHAFFSSTTLDDIILHAFSEVSAARVVGYYLIMLAYACVTLRWDCAQ 420
Db	361 QLAQEALPENASQOIHAFFSSTTLDDIILHAFSEVSAARVVGYYLIMLAYACVTLRWDCAQ 420
Qy	421 SGQSVGLAGVLLVALAVASGLIGLCALLGITFNATTOVLFFLALGIGVDVFLLAHAFTE 480
Db	421 SGQSVGLAGVLLVALAVASGLIGLCALLGITFNATTOVLFFLALGIGVDVFLLAHAFTE 480

```
Qy 481 ALPGTPIQRMGECLQRTGTSTVLTSTINNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
Db 481 ALPGTPIQRMGECLQRTGTSTVLTSTINNMAAFMAALVPIPALRAFSLQAAIVVGCTFV 540
Qy 541 AVMLVFPAILSLDRLRRHRCQRLDVLCCFSSPCSAQVQIQLPOELGDDGTVPVGINAHLTATV 600
Db 541 AVMLVFPAILSLDRLRRHRCQRLDVLCCFSSPCSAQVQIQLPOELGDDGTVPVGINAHLTATV 600
Qy 601 QAFTHCEASSQHVVTILPPQAHVLVPPSPDPLGSELFSFGGSTRDLLGOEBETROKAAACKS 660
Db 601 QAFTHCEASSQHVVTILPPQAHVLVPPSPDPLGSELFSFGGSTRDLLGOEBETROKAAACKS 660
Qy 661 LPCARNWLAHPARYQFAPLLQSHAKAIVLVLCALLGLSLYGATLVQDGLALTDVVVPRG 720
Db 661 LPCARNWLAHPARYQFAPLLQSHAKAIVLVLCALLGLSLYGATLVQDGLALTDVVVPRG 720
Qy 721 TKEHAFLSAQLRYESLVEVALVTGGFDYAHSQBALFDLHQRFSSLKAVLPPPATQAPRT 780
Db 721 TKEHAFLSAQLRYESLVEVALVTGGFDYAHSQBALFDLHQRFSSLKAVLPPPATQAPRT 780
Qy 781 WLHYRWNWLOGIQAAFQDQWASGRITRHSYRNGSEGDGALAYKLLIQTDGAQEPDLDFSQLT 840
Db 781 WLHYRWNWLOGIQAAFQDQWASGRITRHSYRNGSEGDGALAYKLLIQTDGAQEPDLDFSQLT 840
Qy 841 TRKLVDRGLIPPELFYMGFTVWVYSDPLGLAASQANFYPPPPPEWLHDKYDTTGENLRIP 900
Db 841 TRKLVDRGLIPPELFYMGFTVWVYSDPLGLAASQANFYPPPPPEWLHDKYDTTGENLRIP 900
Qy 901 PAQPLEFAQPPFLRLGLOKTDADFVEAIEGARAACAEGAGVHAYPGSGPFLFWEQVLGL 960
Db 901 PAQPLEFAQPPFLRLGLOKTDADFVEAIEGARAACAEGAGVHAYPGSGPFLFWEQVLGL 960
Qy 961 RRCFLAVLCILVCTELVCALLLNPNMTAGLILVLAMVTVELFGINGELGKLSAIPVV 1020
Db 961 RRCFLAVLCILVCTELVCALLLNPNMTAGLILVLAMVTVELFGINGELGKLSAIPVV 1020
Qy 1021 ILVASVGIGVEFTVHVALGFTTQGSRLNRAHALEHTFAPVTDGAI STLGLLMLAGSH 1080
Db 1021 ILVASVGIGVEFTVHVALGFTTQGSRLNRAHALEHTFAPVTDGAI STLGLLMLAGSH 1080
Qy 1081 FDFIVRYFFAALTITLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPOGGG 1140
Db 1081 FDFIVRYFFAALTITLLGLLHGLVLLPVLLSILGPPPEVIOMYKESPEILSPAPOGGG 1140
Qy 1141 LRWGASSSLPQSFARVTTMTVAITHPPPLPGAYIHPAPDEPPSPAAATSSGNLSRGGPG 1200
Db 1141 LRWGASSSLPQSFARVTTMTVAITHPPPLPGAYIHPAPDEPPSPAAATSSGNLSRGGPG 1200
Qy 1201 ATG 1203
Db 1201 ATG 1203

RESULT 4
AY28444
ID AY28444 standard; protein; 1203 AA.
XX
AC AY28444;
XX
XX AY28444;
XX
DT 03-DEC-1999 (first entry)
XX
DE Human ptc-2 protein.
XX
KW Patched-2; ptc-2; human; hedgehog receptor; nontropic; neuroprotective;
KW antiinflammatory; antiparkinsonian; cardiant; antiarthritic; screening;
KW modulator; antagonist; agonist; cellular proliferation; neuronal tissue;
KW testicular tissue; osteogenic tissue; chondrogenic tissue; disease;
KW graft; transplant; treatment; nervous system injury; chemical injury;
KW nasal injury; infection; inflammatory; tumor-induced injury; ageing;
KW Alzheimer's disease; chronic neurodegenerative disease; innervation;
KW Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
KW spinocerebellar degeneration; multiple sclerosis; autonomic disorders;
KW peripheral nervous system; smooth muscle; endocrine tissue; tachycardia;
```

```
KW atrial cardiac arrhythmia; cell differentiation; chronic pain syndrome;
KW lesion-induced death; neuron regeneration; damage repair; skeletal;
KW cartilage; osteogenesis; arthritis; bone fracture; hereditary disease;
KW prosthetic cartilage device; spermatogenesis; fertility enhancer.
XX Homo sapiens.
XX WO929854-A1.
XX
XX 17-JUN-1999.
XX
XX 08-DEC-1998; 98WO-US026009.
XX
XX 08-DEC-1997; 97US-0067940P.
XX
XX (ONTO-) ONTOGENY INC.
XX
XX Bumcrot DA;
XX
XX WPI; 1999-561298/47.
XX N-PSDB; AAX89478.
XX
XX New human patched-2 (ptc-2) genes and proteins, useful in the treatment,
XX prevention and/or reduction of the severity of neurological conditions.
XX
XX Claim 3; Page 73-77; 80pp; English.
XX
XX This invention describes a novel recombinantly produced human patched-2
XX (ptc-2) polypeptide which has nontropic, neuroprotective, cardiant,
XX antiinflammatory, antiparkinsonian and antiarthritic activity. The ptc-2
XX protein is a hedgehog receptor and is therefore capable of modulating
XX hedgehog signalling, and so affect a number of hedgehog-mediated
XX biological activities. The human patched-2 (ptc-2) protein can be used to
XX screen for modulators, antagonists and agonists, which are likely to play
XX an important role in the modulation of cellular proliferation and
XX maintenance of, e.g. neuronal, testicular, osteogenic or chondrogenic
XX tissues during disease states. Modulators of ptc-2 protein can be used
XX for in vivo reformation of tissue; to improve grafting and morphology of
XX transplanted tissue; for the treatment, prevention and/or reduction of
XX the severity of neurological conditions deriving from: injury to the
XX nervous system including traumatic injury, chemical injury, vascular injury
XX and deficits (such as ischemia resulting from stroke), together with
XX infectious/inflammatory and tumor-induced injury; ageing of the nervous
XX system including Alzheimer's disease; chronic neurodegenerative diseases
XX of the nervous system including Parkinson's disease, Huntington's chorea,
XX and chronic immunological diseases of the nervous system including
XX amyotrophic lateral sclerosis, as well as spinocerebellar degenerations;
XX multiple sclerosis. ptc-2 therapeutics can also be used in the treatment
XX of autonomic disorders of the peripheral nervous system, including
XX disorders affecting the innervation of smooth muscle and endocrine
XX tissue, e.g. to treat tachycardia or atrial cardiac arrhythmias.
XX Antagonists of ptc-2 protein can be used to prevent differentiation of
XX cells in culture, as well as for treatment of chronic pain syndromes.
XX Agonists may be used to rescue neurons from lesion-induced death as well
XX as neuron regeneration, in diseases such as CNS trauma infarction, (viral)
XX infection, metabolic disease, nutritional deficiency, toxic agents, and
XX so on. ptc-2 therapeutics may also be used for the repair of central and
XX peripheral nerve damage, for repair and regeneration of non-neuronal
XX tissue, e.g. skeletal and cartilage tissue, e.g. in the treatment of
XX osteogenesis, arthritis, bone fractures, hereditary disease, as well as
XX for generation of prosthetic cartilage devices, and to induce
XX spermatogenesis and as fertility enhancers. This sequence represents the
XX human ptc-2 protein described in the invention
XX
XX Sequence 1203 AA;
```

```
Query Match 74.8%; Score 900; DB 2; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MTRSPPLRLPSPYTPPARTAAQIILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCKVLF 60
Db 1 MTRSPPLRLPSPYTPPARTAAQIILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCKVLF 60
```


QY 1 MTRSPPLRELPPSYTPPARTAAPOTILAGSLKAPLWLRAYFOGILLFSLGCGIORHCGKVL 60
DB 1 MTRSPPLRELPPSYTPPARTAAPOTILAGSLKAPLWLRAYFOGILLFSLGCGIORHCGKVL 60
QY 61 LGLAFAGALAGLMAIITETNLEQLWVEVGRSVQELHYTKELGEBAAATYSQMLIQ 120
DB 61 LGLAFAGALAGLMAIITETNLEQLWVEVGRSVQELHYTKELGEBAAATYSQMLIQ 120
QY 121 QEGENILTPALGHLQALATASKVOVSLYKSDNLANKICYKSGVPLIENGMIEMIEKL 180
DB 121 QEGENILTPALGHLQALATASKVOVSLYKSDNLANKICYKSGVPLIENGMIEMIEKL 180
QY 181 FPCVILTPDCFWEGAKLOGGSAYLPGRPDTQWNLDPQELLEBELGFPASLEGFRELDDK 240
DB 181 FPCVILTPDCFWEGAKLOGGSAYLPGRPDTQWNLDPQELLEBELGFPASLEGFRELDDK 240
QY 241 AQVQAVYGRPCPLHPDDLHCPPSPAPNHHSRQAPNVAHELSCGCHGFSGHKFMHQBELLG 300
DB 241 AQVQAVYGRPCPLHPDDLHCPPSPAPNHHSRQAPNVAHELSCGCHGFSGHKFMHQBELLG 300
QY 301 GMARDPOGELURAEALSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLQAWQRFFV 360
DB 301 GMARDPOGELURAEALSTFLLMSPROLYEHFRGDYQTHDIGWSEEOASTVLQAWQRFFV 360
QY 361 QLAQEAALPENASQOIHAFSSTLDDILHAFSEVAARVVGGLYLLMLAYACVTMLRWDCAQ 420
DB 361 QLAQEAALPENASQOIHAFSSTLDDILHAFSEVAARVVGGLYLLMLAYACVTMLRWDCAQ 420
QY 421 SQSGVGLAGVLLVALAVASGLGALLGITFNAATQVLPFLALGIGVDDVFLAHAFTE 480
DB 421 SQSGVGLAGVLLVALAVASGLGALLGITFNAATQVLPFLALGIGVDDVFLAHAFTE 480
QY 481 ALPGTPIQERMGECLQRTGTSVLTSTINNMAAFMAALVPTPALRAFSLQAAIIVGCTFV 540
DB 481 ALPGTPIQERMGECLQRTGTSVLTSTINNMAAFMAALVPTPALRAFSLQAAIIVGCTFV 540
QY 541 AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVIQILPOELGDDGTPVPGIAHLATV 600
DB 541 AVMLVFPAILSLDLRRHRCORLDVLCFSPSCSAQVIQILPOELGDDGTPVPGIAHLATV 600
QY 601 QAFTHCEASSQHVVTILPQOHLVPPSPDPLGSELFSFGGSTRDLGQEBETROKAAKS 660
DB 601 QAFTHCEASSQHVVTILPQOHLVPPSPDPLGSELFSFGGSTRDLGQEBETROKAAKS 660
QY 661 LPCARWNLHAFARYQFAPLLOSHAKAIVLVFQALLGSLYGATLVQDGLALTDVVPRG 720
DB 661 LPCARWNLHAFARYQFAPLLOSHAKAIVLVFQALLGSLYGATLVQDGLALTDVVPRG 720
QY 721 TKEHAFLSAQLRYFSLYEVALVTOGGFDYAHQSORALFDLHORFSSKAVLPPPPATQAPRT 780
DB 721 TKEHAFLSAQLRYFSLYEVALVTOGGFDYAHQSORALFDLHORFSSKAVLPPPPATQAPRT 780
QY 781 WLHYRNWLOGIQAFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTDGAQEPDLFSQLT 840
DB 781 WLHYRNWLOGIQAFQDQWASGRITRHSYRNGSEDEGALAYKLLIQTDGAQEPDLFSQLT 840
QY 841 TRKLVDREGLIPPELFYGLTWVSSDPLGLAASQANFYPPPPHWDKDYDTTGENRIP 900
DB 841 TRKLVDREGLIPPELFYGLTWVSSDPLGLAASQANFYPPPPHWDKDYDTTGENRIP 900
QY 901 PAQPLEFAQPFLLRGLQKTDADFEATEGARACAEAGVHAYPSGSPFLFWEQYGL 960
DB 901 PAQPLEFAQPFLLRGLQKTDADFEATEGARACAEAGVHAYPSGSPFLFWEQYGL 960
QY 961 RRCFLAVCILLVCTFLVLCALLLNPTAGILVILVAMTVELFGINGFLGKLSAIPV 1020
DB 961 RRCFLAVCILLVCTFLVLCALLLNPTAGILVILVAMTVELFGINGFLGKLSAIPV 1020
QY 1021 ILVASVIGVEFTVHVALGFLTTQGSNRNLRAHALEHTFAPVTDGAIISTLLGLMLAGSH 1080
DB 1021 ILVASVIGVEFTVHVALGFLTTQGSNRNLRAHALEHTFAPVTDGAIISTLLGLMLAGSH 1080

QY 1081 FDTIVRFFAALTVLTLLGLHGLVLLPVLSSILGPPPEVIQMYKESPEILSPAPQGG 1140
DB 1081 FDTIVRFFAALTVLTLLGLHGLVLLPVLSSILGPPPEVIQMYKESPEILSPAPQGG 1140
QY 1141 LRWGASSSLPQSFARVTTSTMTVAIHPPPLPGAYIHPADPPPMSPAAATSSG 1191
DB 1141 LRWGASSSLPQSFARVTTSTMTVAIHPPPLPGAYIHPADPPPMSPAAATSSG 1191
RESULT 6
AA92225
ID AAY92225 standard; protein; 1146 AA.
XX AAY92225;
XX AC AC
XX DE DE
DT 10-AUG-2000 (first entry)
XX Human patched 2 (PTCH2) protein.
XX Patched 2; PTCH2; tumour suppressor; familial melanoma CM1;
KW familial adenomatous polyposis; hMcm1; Michelin Tire Baby Syndrome;
KW sonic hedgehog; SHH; development; carcinogenesis; cycostatic;
KW basal cell carcinoma; chromosome 1p32-35; gene therapy.
XX Homo sapiens.
OS
XX W0200020037-A1.
PN
XX 13-APR-2000.
PD
XX 06-OCT-1999; 99WO-SB001784.
PF
XX 06-OCT-1998; 98SE-00003393.
PR
XX (KARO-) KAROLINSKA INNOVATIONS AB.
PA (PHAA) PHARMACIA & UPJOHN CO.
PA
XX Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;
PI Hollingsworth RE;
PI
DR WPI; 2000-303645/26.
XX N-PSDB; AAA09081, AAA09084.
XX Isolated human protein capable of participating in human patched
PT gene/sonic hedgehog pathway during embryonic development is used in
PT medicament for treatment of condition involving tumors such as basal cell
PT carcinoma.
XX
PS Claim 2; Page 41-44; 55pp; English.
XX
CC This protein is encoded by the novel human patched 2 gene (PTCH2), which
CC has been localised by radiation hybrid mapping to chromosome 1p32-35 with
CC DIS211 and Wil404 as closest flanking markers and with an estimated
CC localisation 5.5 cR from DIS443. This region is often lost by LOH in
CC various different tumour types, such as neuroblastoma, melanoma and
CC breast and colon cancer. PTCH2 is a candidate for a tumour suppressor
CC gene in this region. It is also a candidate gene for involvement in
CC familial melanoma CM1, modifier locus for familial adenomatous polyposis
CC hMcm1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene
CC exist (see AAA09082-84). PTCH2 is capable of participating in the human
CC patched gene/sonic hedgehog (PTCH/SHH) pathway during embryonic
CC development and/or carcinogenesis. The isolated human protein is useful
CC as a medicament for the treatment of a condition involving tumours such
CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene
CC therapy, and for use as a probe, primer or a diagnostic agent
XX
SQ Sequence 1146 AA;
Query Match 69.7%; Score 839; DB 3; Length 1146;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1139; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIORHCGKVL 60

	Db	1081	FDFIVRYFFAALTATVLTLLGLLHGLVLLPVLSILSGPPPEVIQWKSPSEILSPPAPOGGG	1141 LR 1142	1141 LR 1142	1141 LR 1142	RESULT 7 AAW82586 ID AAW82586 standard; protein; 529 AA. XX AAW82586; AC AAW82586; XX XX DT 01-MAR-1999 (first entry) XX Human Patched-2 protein. DE Patched-2; human; patched receptor; diagnosis; disease; screening; XX immune response; immunise; vaccine; inoculation; treatment; cancer; KW kidney diseases; cardiovascular disease; stroke; inflammatory disorder; KW neurological disorder; Alzheimer's disease; Prosis; gene mapping; KW linkage analysis; tissue localisation. XX Homo sapiens. OS XX EP879888-A2. PN XX 25-NOV-1998. PD XX 20-MAY-1998; 98EP-00303994. PF XX 23-MAY-1997; 97GB-00010752. PR 19-MAR-1998; 98GB-00005954. PR XX (SMIK) SMITHKLINE BEECHAM PLC. PA XX Kelsell DP, Barnes MR, Testa TT; PI WPI; 1998-596880/51. XX N-PSDB; AAV69382. DR XX New Patched-2 polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of Alzheimer's disease, cancer and strokes. PT XX Claim 3; Page 17-19; 27pp; English. PS XX This sequence represents a human patched receptor (Patched-2) polypeptide. Patched-2 polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the Patched-2 gene and can diagnose diseases associated with Patched-2 imbalance. Patched-2 polypeptides can be used to screen for agonists and antagonists which bind the polypeptide by detecting patched-2 mRNA levels in ELISA assays. These can be used in treatment to activate (agonist) or inhibit (antagonist) Patched-2 activity. Patched-2 antibodies are useful for inducing an immune response to immunise and prevent diseases and for isolating Patched-2 clones or purifying the polypeptides by affinity chromatography. Patched-2 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases diagnosed, prevented or treated include cancer, kidney diseases, cardiovascular disease, stroke, inflammatory disorders, neurological disorders including Alzheimer's disease and mood disorders and developmental disorders including Prosis. The Patched-2 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis. Patched-2 polynucleotides may be useful in tissue localisation studies e.g. in situ hybridisations, to determine expression patterns and indicate normal functions of the polypeptide in vivo CC XX Sequence 529 AA;
	Qy	Query Match	41.3%; Score 497; DB 2; Length 529;				
	Db	Best Local Similarity	100.0%; Pred. No. 0;				
		Matches 497; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				

QY 491 MGECLQRTGTSVLTSTNNMAAFMAALPIPALRAFSLOAAIYVVGCTFVAVMLVFPAIL 550
 DB 1 MGECLQRTGTSVLTSTNNMAAFMAALPIPALRAFSLOAAIYVVGCTFVAVMLVFPAIL 60
 QY 551 SLDLRRHCQRLDVLCCFSSPCSAQVILPQELGDTGTPVGVIAHLTATVQAFTHCEASS 610
 DB 61 SLDLRRHCQRLDVLCCFSSPCSAQVILPQELGDTGTPVGVIAHLTATVQAFTHCEASS 120
 QY 611 QHVVTLIPPOAHLVPPSPDPLGSELSPGSGSTRLLGQEBETROKAAKSLPCARWNLAH 670
 DB 121 QHVVTLIPPOAHLVPPSPDPLGSELSPGSGSTRLLGQEBETROKAAKSLPCARWNLAH 180
 QY 671 FARYQFAPLLQSHAKAIVLVLFGLLGLSLYGATLVQDGLALTDVVPRTGKHAFLSAQ 730
 DB 181 FARYQFAPLLQSHAKAIVLVLFGLLGLSLYGATLVQDGLALTDVVPRTGKHAFLSAQ 240
 QY 731 LRYFSLYEVALVTGGFDYAHSQRALFDLHORFSSLKAVLPPPPATQAPRTWLHYRNWLQ 790
 DB 241 LRYFSLYEVALVTGGFDYAHSQRALFDLHORFSSLKAVLPPPPATQAPRTWLHYRNWLQ 300
 QY 791 GIOAEPDQDASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPDLFSQLTRKLVDREGL 850
 DB 301 GIOAEPDQDASGRITRHSYRNGSEDCALAYKLLIQTGDAQEPDLFSQLTRKLVDREGL 360
 QY 851 IPPELFYMGTLVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIPPAQLEPAQF 910
 DB 361 IPPELFYMGTLVWVSSDPLGLAASQANFYPPPEWLHDKYDTTGENLRIPPAQLEPAQF 420
 QY 911 PFLRLGLOKTDVFEATEGARAAEAGAGVHAYPSGSPFLFWEQYGLRRCFLAVCI 970
 DB 421 PFLRLGLOKTDVFEATEGARAAEAGAGVHAYPSGSPFLFWEQYGLRRCFLAVCI 480
 QY 971 LLVCTFLVCALLLNWP 987
 DB 481 LLVCTFLVCALLLNWP 497
 RESULT 8
 AAE19831
 ID AAE19831 standard; protein; 1182 AA.
 AC AAE19831;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Mouse patched-2 (Ptc-2) protein.
 XX
 KW Mouse; patched-2; Ptc-2; cell proliferation; differentiation; therapy;
 KW cytostatic; testicular cancer; hedgehog protein signalling.
 XX
 OS Mus musculus.
 XX
 PN US6348575-B1.
 XX
 PD 19-FEB-2002.
 XX
 PF 15-APR-1999; 99US-00293505.
 XX
 PR 15-APR-1998; 98US-0081884P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI De Sauvage F, Carpenter DA;
 XX
 DR WPI; 2002-215260/27.
 XX
 CC Native human patched-2 polypeptide for treating disorders caused by
 PT Hedgehog protein signalling such as testicular cancer, and for screening
 PT cDNA libraries.
 XX
 PS Example 1; Fig 8; 82pp; English.

CC The invention relates to an isolated sequence comprising a native human
 CC patched-2 (Ptc-2) polypeptide. The invention also relates to signalling
 CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
 CC cell proliferation and differentiation. The isolated sequence is useful
 CC for the treatment of disorders which are linked to hedgehog, especially
 CC Desert hedgehog expression, such as testicular cancer. It may also be
 CC used as a hybridisation probe in a cDNA library to isolate Ptc-2 or its
 CC homologues, and to diagnose whether a disorder is driven by Ptc-2 or
 CC Hedgehog protein signalling. The present sequence is mouse patched-2
 CC (Ptc-2) protein
 XX
 SQ Sequence 1182 AA;
 Query Match 7.8%; Score 94; DB 5; Length 1182;
 Best Local Similarity 100.0%; Pred. No. 1.1e-80;
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 693 FGALLGLSLYGATLVQDGLALTDVVPRTGKHAFLSAQLRYFSLYEVALVTGGFDYAH 752
 DB 693 FGALLGLSLYGATLVQDGLALTDVVPRTGKHAFLSAQLRYFSLYEVALVTGGFDYAH 752
 QY 753 ORALFDLHORFSSLKAVLPPPPATQAPRTWLHYR 786
 DB 753 ORALFDLHORFSSLKAVLPPPPATQAPRTWLHYR 786
 RESULT 9
 AAW82587
 ID AAW82587 standard; protein; 46 AA.
 XX
 AC AAW82587;
 XX
 DT 01-MAR-1999 (first entry)
 XX
 DE Human Patched-2 EST HNFIR49 protein.
 XX
 KW Patched-2; human; patched receptor; diagnosis; disease; screening;
 KW immune response; immunise; vaccine; inoculation; treatment; cancer;
 KW kidney diseases; cardiovascular disease; stroke; inflammatory disorder;
 KW neurological disorder; Alzheimer's disease; Ptois; gene mapping;
 KW linkage analysis; tissue localisation; expressed sequence tag; EST.
 XX
 OS Homo sapiens.
 XX
 PN EP879888-A2.
 XX
 PD 25-NOV-1998.
 XX
 PF 20-MAY-1998; 98EP-00303994.
 XX
 PR 23-MAY-1997; 97GB-00010752.
 PR 19-MAR-1998; 98GB-00005954.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Kelsell DP, Barnes MR, Testa TT;
 XX
 DR WPI; 1998-596880/51.
 DR N-PSDB; AAV69383.
 XX
 PT New Patched-2 polypeptide and polynucleotide - useful as diagnostic
 PT reagents and for prevention and treatment of Alzheimer's disease, cancer
 PT and strokes.
 XX
 PS Claim 19c; Page 19; 27pp; English.
 XX
 CC This sequence represents a human patched receptor (Patched-2) expressed
 CC sequence tag (EST) fragment HNFIR49. Patched-2 polypeptides and
 CC polynucleotides are useful for diagnosing susceptibility to diseases by
 CC detecting mutations in the Patched-2 gene and can diagnose diseases
 CC associated with Patched-2 imbalance. Patched-2 polypeptides can be used
 CC to screen for agonists and antagonists which bind the polypeptide by
 CC detecting Patched-2 mRNA levels in ELISA assays. These can be used in

CC treatment to activate (agonist) or inhibit (antagonist) Patched-2
 CC activity. Patched-2 antibodies are useful for inducing an immune response
 CC to immunise and prevent diseases and for isolating Patched-2 clones or
 CC purifying the polypeptides by affinity chromatography. Patched-2
 CC polypeptides can be administered directly or as a vaccine to inoculate
 CC against disease. Diseases diagnosed, prevented or treated include cancer,
 CC kidney diseases, cardiovascular disease, stroke, inflammatory disorders,
 CC neurological disorders including Alzheimer's disease and mood disorders,
 CC and developmental disorders including Ptois. The Patched-2 polypeptide
 CC is also useful for mapping the gene to a chromosome, allowing gene
 CC inheritance to be studied through linkage analysis. Patched-2
 CC polynucleotides may be useful in tissue localisation studies e.g. in situ
 CC hybridisations, to determine expression patterns and indicate normal
 CC functions of the polypeptide in vivo
 XX
 SQ Sequence 46 AA;

Query Match 3.6%; Score 43; DB 2; Length 46;
 Best Local Similarity 100.0%; Pred. No. 8.5e-33;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 488 QERMGECLQRTGTSVLTSSINNAFLMAALVPIPALRAFSLQ 530
 |||||
 Db 4 QERMGECLQRTGTSVLTSSINNAFLMAALVPIPALRAFSLQ 46

RESULT 10
 AAO01960
 ID AAO01960 standard; protein; 119 AA.

XX AAO01960;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 15852.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AA181891.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 15852; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or

CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 119 AA;

Query Match 2.7%; Score 32; DB 4; Length 119;

Best Local Similarity 100.0%; Pred. No. 7.7e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 457 QVLFFLALGIGVDDVFLLAHAFTEALPGTFLQ 488
 |||||
 Db 33 QVLFFLALGIGVDDVFLLAHAFTEALPGTFLQ 64

RESULT 11

ADD46676

ID ADD46676 standard; protein; 608 AA.

XX ADD46676;

XX 02-DEC-2004 (revised)

XX 29-JAN-2004 (first entry)

XX Rat Protein AAC99398, SEQ ID NO 12361.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX Unidentified.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; AAC99398.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Example 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 608 AA;

Query Match 1.2%; Score 15; DB 7; Length 608;
 Best Local Similarity 100.0%; Pred. No. 7.6e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
 |||||
 Db 481 FNAATTQVLPLALG 495

RESULT 12
 AA47157
 ID AA47157 standard; protein; 1296 AA.

XX AA47157;

XX 27-MAY-1998 (first entry)

XX Nevoid basal cell carcinoma syndrome (NBCCS) (PTC) protein.

XX Nevoid basal cell carcinoma syndrome; NBCCS; PTC; PATCHED; detection;
 KW tumour suppressor; human; mutation; Gorlin's syndrome.

XX Homo sapiens.

XX WO9743414-A2.

XX 20-NOV-1997.

XX 16-MAY-1997; 97WO-US008433.

XX 17-MAY-1996; 96US-0017906P.

XX 21-MAY-1996; 96AU-00000011.

XX 07-JUN-1996; 96AU-00000363.

XX 14-JUN-1996; 96US-0019765P.

XX 16-MAY-1997; 97US-00857636.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Dean MF, Hahn H, Wicking C, Christiansen J, Zaphiropoulos PG;

XX Gallani MR, Shanley S, Chidambaram A, Vorechovsky I, Holmberg E;

XX Unden AB, Gillies S, Negus K, Smyth I, Pressman C, Lefell DJ;

XX Gerrard B, Goldstein A, Wainwright B, Toftgard R, Chevenix-Trench G;

XX WPI; 1998-008883/01.

XX N-PSDB; AAV15949.

XX Nevoid basal cell carcinoma syndrome tumour suppressor gene - useful for
 PT detection of pre-disposition to basal cell carcinoma(s).

XX Disclosure; Fig 8; 148pp; English.

XX This is a nevoid basal cell carcinoma syndrome (NBCCS) (PTC) protein. The
 CC encoding nucleic acid specifically hybridises, under stringent
 CC conditions, to a second nucleic acid consisting of a 6568 (full-length
 CC sequence), 1732 (exon 1a, b) (AAV15998) or 659 (exon 2a) (AAV15999) base
 CC pair sequence, in the presence of a human genomic library. The PTC
 CC polypeptide when presented as an antigen elicits the production of an
 CC antibody which specifically binds to a polypeptide encoded by the above
 CC three sequences. The NBCCS gene and its protein product, is a tumour
 CC suppressor, and is a homologue of the Drosophila PATCHED (PTC) gene.

CC Detection of the NBCCS nucleic acid, in particular abnormal sequences, by
 CC hybridisation assays is useful for detecting a predisposition to NBCCS or
 CC to a basal cell carcinoma (also known as Gorlin syndrome). Alternatively,
 CC detection is of the polypeptide and is carried out by immunoassay.
 CC Vectors comprising this nucleic acid can be used to treat NBCCS. The PTC
 CC polypeptide can mitigate symptoms of NBCCS in an organism. The NBCCS
 CC nucleic acid includes one or more mutations, chosen from Exon-5 693insC,
 CC Exon-17 298del8bp, Exon-21 353delG, Exon-22 G4302T, Exon-12 1711insC,
 CC Exon-12 1639insA, Exon-16 2707delC, and Intron-17 3157-2A to G. The
 CC mutation may be a nonsense or frameshift mutation. Frameshift mutations
 CC are chosen from 244delCT, 271insA, 464insAC, 693insC, 804del137, 877delG,
 CC 929delC, 1370del176, 1393insTGCC, 1444del16, 1497dup8, 1639insA, 1711insC,
 CC 2183delTC, 2320insTC, 2392delA, 2574delA, 2583delC, 2596complex,
 CC 2707delC, 2748insC, 2749dup7, 2988del8bp, 3014insA, 3352delAT and
 CC 3338delG. The mutation may be a missense, chosen from G391T, G1148A,
 CC G1368A, G1525T, C2050T, C2068T, C3015A, G3193C AND G4302T. Alternatively,
 CC the mutation alters mRNA splicing and is chosen from A1055-2C, 3157-2A to
 CC G and 1493-8ins21. All these mutations are claimed but their sequences
 CC are not provided in the specification
 XX SQ Sequence 1296 AA;

Query Match 1.2%; Score 15; DB 2; Length 1296;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
 |||||
 Db 344 FNAATTQVLPLALG 358

RESULT 13

AA94380

ID AA94380 standard; protein; 1434 AA.

XX AA94380;

XX 11-JUL-1996 (first entry)

XX Mouse patched protein.

XX Patched gene; PTC protein; embryo development; cellular regulation;
 KW signal transduction; ligand; antibody; hedgehog protein.

XX Mus musculus.

XX WO9611260-A1.

XX 18-APR-1996.

XX 06-OCT-1995; 95WO-US013233.

XX 07-OCT-1994; 94US-00319745.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Scott MP, Goodrich LV, Johnson RL;

XX WPI; 1996-209842/21.

XX N-PSDB; AAT14218.

XX DNA encoding patched protein other than Drosophila patched protein - used
 PT to produce antibodies which detect or inhibit patched protein ligand
 PT signal transduction in cells.

XX Disclosure; Page 46-51; 70pp; English.

XX Mouse patched protein (PTC) (AA94380) was identified as the product of a
 CC cDNA clone (AA114218) derived from mouse limb bud. It has about 38%
 CC identical amino acids to Drosophila PTC. PTC protein has been proposed as
 CC a receptor for hedgehog protein on basis of genetic experiments in flies.
 CC Murine PTC protein can be obtd. in large amounts by expression of the
 CC cDNA clone in transfected host cells. It can be used to screen for

CC agonists and antagonists, to isolate its ligand, partic. Sonic hedgehog,
 CC to assay for the transcription of ptc mRNA and to raise antibodies
 XX
 XX
 SQ Sequence 1434 AA;

Query Match 1.2%; Score 15; DB 2; Length 1434;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 481 FNAATTQVLPLALG 495

RESULT 14
 AAW52199
 ID AAW52199 standard; protein; 1434 AA.

XX AAW52199;

AC AAW52199;

XX 25-JUN-1998 (first entry)

DT Mouse patched (ptc) protein.

DE Mouse patched (ptc) protein.

XX Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter;

KW wound healing; ageing; mouse.

XX Mus sp.

OS WO9745541-A2.

PN 04-DEC-1997.

XX 02-JUN-1997; 97WO-US009553.

XX 31-MAY-1996; 96US-00656055.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

PA (REGC) UNIV CALIFORNIA.

XX Scott MP, Goodrich LV, Johnson RL, Epstein E, Oro A;

PI WPI; 1998-032648/03.

DR N-PSDB; AAV21589.

XX Patched protein other than Drosophila melanogaster patched protein - used

PT for characterising the phenotype of a tumour.

XX Claim 5; Page 66-71; 86pp; English.

PS This is a mouse patched (ptc) protein. The encoding DNA can be used to

CC construct an expression cassette comprising an altered patch or hedgehog

CC gene. The expression cassette comprises a nucleic acid encoding a patched

CC protein other than a Drosophila melanogaster patched protein, or fragment

CC of at least 12 nucleotides in length, as other than an intact chromosome

CC under transcriptional control of a transcriptional initiation region, and

CC a transcriptional termination region, both functional in an expression

CC host. A genetically engineered mammalian cell comprising this expression

CC cassette as an extrachromosomal element or integrated into the genome of

CC the cell can be predisposed to develop basal cell carcinoma as a result

CC of the transfection. By analysing DNA, functional analysis of patched

CC protein function, or by detecting antibody binding to abnormal patched

CC protein, a genetic predisposition to developmental abnormalities and

CC cancer can be diagnosed. This analysis can also be used for

CC characterising the phenotype of a tumour, particularly a carcinoma,

CC especially a basal cell carcinoma. The methods can also be used for

CC characterising transitional cell carcinoma of the bladder, meningiomas

CC medulloblastomas, etc. The modified cells comprising the expression

CC cassette can be used to determine the role of different exons of the

CC patched gene in oncogenesis, signal transduction, etc. Transgenic animal

CC models created from these cells can be used as animal models for

CC carcinomas of the skin. The patched protein of mosquito, butterfly or

CC beetle or alternatively, a mammalian patched protein of human or mouse

CC can be used to identify ligands or substrates that bind to, modulate, or
 CC mimic the action of patched gene. These agents could be used as tumour
 XX suppressors, cell adhesion promoters (e.g. in wound healing and ageing)
 XX
 SQ Sequence 1434 AA;

Query Match 1.2%; Score 15; DB 2; Length 1434;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 481 FNAATTQVLPLALG 495

RESULT 15
 AAW72968
 ID AAW72968 standard; protein; 1434 AA.

XX AAW72968;

AC AAW72968;

XX 26-JAN-1999 (first entry)

DT Mouse patched protein.

DE Mouse patched protein.

XX Mouse; patched gene; diagnosis; treatment; developmental disorder;

KW cancer; healing; injured tissue; ptc; spina bifida; Wnt-1 oncogene;

KW sperm production; gene therapy.

XX Mus sp.

XX US5837538-A.

PN 17-NOV-1998.

XX 06-OCT-1995; 95US-00540406.

XX 07-OCT-1994; 94US-00319745.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

PA Scott MP, Goodrich LV, Johnson RL;

PI WPI; 1999-023461/02.

DR N-PSDB; AAV64092.

XX Nucleic acid encoding vertebrate patched protein and related

PT transformants - used to express poly:peptide(s), useful for diagnosis and

PT treatment of developmental disorders or cancer, and in healing of injured

PT tissue.

XX Claim 23; Col 49-56; 38pp; English.

PS The present sequence represents the mouse patched (ptc) protein. Cells

CC containing and expressing the ptc gene are used for the recombinant

CC production of the protein. These in turn are useful: (i) for generating

CC antibodies (Ab); and (ii) to screen for specific-binding ligands

CC (potential therapeutic agonists and antagonists). The ptc gene, or its

CC fragments, are used to isolate related sequences from other mammals; to

CC identify mutations (particularly those associated with genetic diseases

CC such as spina bifida and other developmental disorders); to monitor

CC expression levels in testis (to determine relationship with sperm

CC production) and to isolate 5'-non-coding sequences (used to study

CC embryonic development and to provide regulated expression of proteins).

CC The complete gene can be used in gene therapy, including expression of

CC antisense molecules, and to generate transgenic animals for studies of

CC embryonic development. Ab are used diagnostically to determine the ptc

CC protein on cell surfaces and as competitive inhibitors of signal

CC transduction through the ptc ligand. Cells that have been engineered to

CC express the ptc protein can be used to promote regrowth and healing of

CC damaged tissue (e.g. growth of new teeth) and regulation of the ptc

CC protein expression may be useful in cancer treatment (it may control the

CC Wnt-1 oncogene)

```

XX SQ Sequence 1434 AA;
Query Match 1.2%; Score 15; DB 2; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
  |||||
DB 481 FNAATTQVLPLALG 495

RESULT 16
AAB67159
ID AAB67159 standard; protein; 1434 AA.
XX
AC AAB67159;
XX
DT 12-APR-2001 (first entry)
XX
DE Murine patched protein.
XX
KW Mouse; patched; PTC; segment polarity; limb patterning; development;
KW hedgehog; antibody; human.
XX
OS Mus sp.
XX
PN US6172200-B1.
XX
PD 09-JAN-2001.
XX
PF 20-OCT-1997; 97US-00954668.
XX
PR 07-OCT-1994; 94US-00319745.
PR 06-OCT-1995; 95US-00540406.
XX
PA (STRD ) UNIV LELAND S STANFORD.
XX
PI Scott MP, Goodrich LV, Johnson RL;
XX
DR WPI; 2001-136884/14.
DR N-PSDB; AAF32180.
XX
PT Novel monoclonal antibody useful in diagnostic assays for detection of
PT presence of protein on surface of cells specifically binds to naturally
PT occurring patched protein, other than Drosophila patched protein.
XX
PS Disclosure; Col 47-54; 39pp; English.
XX
CC The present invention provides a monoclonal antibody which specifically
CC binds to a patched protein (PTC) other than that from Drosophila. Also
CC given are the protein and coding sequences of patched from the beetle,
CC mouse, butterfly, fruit fly, mosquito and human. Patched is a segment
CC polarity gene involved in limb patterning. The sequences can be used to
CC study development and to isolate the patched ligand, hedgehog. In
CC addition, antibodies can be used to detect the PTC protein on cell
CC surfaces or to inhibit the transduction of signal by the PTC ligand by
CC competing for its binding site
XX
SQ Sequence 1434 AA;
Query Match 1.2%; Score 15; DB 4; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
  |||||
DB 481 FNAATTQVLPLALG 495

RESULT 17
AAG79572
ID AAG79572 standard; protein; 1434 AA.

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XX AAG79572;
XX
DT 23-DEC-2002 (first entry)
XX
DE Mouse patched protein.
XX
KW Patched; ptc; basal cell nevus syndrome; BCNS; wound healing;
KW developmental disorder; spina bifida; craniofacial abnormality;
KW basal cell carcinoma; skin; brain tumour; transgenic; mouse;
KW proliferation; oncogenesis; signal transduction; cancer; aging.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 708
FT /note= "Encoded by TCC"
XX
PN US6429354-B1.
XX
PD 06-AUG-2002.
XX
PF 22-AUG-1997; 97US-00918658.
XX
PR 07-OCT-1994; 94US-00319745.
PR 06-OCT-1995; 95US-00540406.
PR 31-MAY-1996; 96US-00656055.
XX
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PA (REGC ) UNIV CALIFORNIA.
XX
PI Scott MP, Goodrich LV, Johnson RL, Epstein E;
XX
DR WPI; 2002-722086/78.
DR N-PSDB; ABA00375.
XX
PT Transgenic mouse, useful for cancer drug screening, comprises disruption
PT of allele of patched locus which predisposes the mouse to develop a
PT proliferative disorder.
XX
PS Disclosure; Col 69-78; 58pp; English.
XX
CC This sequence shows mouse patched (ptc) protein. Mutations in the patched
CC gene are characteristic in basal cell nevus syndrome (BCNS), an inherited
CC disorder with an increased risk of developmental disorders such as spina
CC bifida and craniofacial abnormalities, basal cell carcinoma of the skin
CC and brain tumours. The human and mouse ptc sequences show 86% homology.
CC The transgenic mouse of the invention has a genome comprising a
CC disruption of at least one allele of a patched locus, where the
CC transgenic mouse is useful for studying patched function and regulation.
CC for e.g. a series of small deletions and/or substitutions made in the
CC patched gene, to determine the role of different exons in oncogenesis,
CC signal transduction, etc; and for drug screening which is useful for
CC treating cancer or developmental abnormalities attributed to a defect in
CC patched function such as wound healing and aging
XX
SQ Sequence 1434 AA;
Query Match 1.2%; Score 15; DB 5; Length 1434;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
  |||||
DB 481 FNAATTQVLPLALG 495

RESULT 18
ABU62271
ID ABU62271 standard; protein; 1434 AA.
XX
AC ABU62271;

```

XX DT 25-AUG-2003 (first entry)
 XX DE Mouse patched gene PTC product.
 XX KW Mouse; patched gene; PTC; hedgehog protein; gene therapy.
 XX OS Mus sp.
 XX PN US2003032085-A1.
 XX PD 13-FEB-2003.
 XX PF 20-OCT-1997; 97US-00954701.
 XX PR 07-OCT-1994; 94US-00319745.
 XX PR 06-OCT-1995; 95US-00540406.
 XX PA (SCOTT/) SCOTT M P.
 XX PA (GOOD/) GOODRICH L V.
 XX PA (JOHN/) JOHNSON R L.
 XX PI Scott MP, Goodrich LV, Johnson RL;
 XX DR WPI; 2003-492065/46.
 XX DR N-PSDB; ACA62834.
 XX PT New DNA sequence other than present in a chromosome encoding patched gene
 XX PT other than Drosophila patched gene, useful for preparing transgenic
 XX PT laboratory animals and to knock out patched protein in embryonic stem
 XX PT cells.
 XX PS Disclosure; Page 8-10; 40pp; English.
 XX CC The invention relates to a DNA sequence other than present in chromosome
 XX CC encoding a patched (ptc) gene other than Drosophila patched gene. A cell
 XX CC expressing the DNA sequence is useful for producing patched protein, by
 XX CC growing the cell expressing the DNA sequence, where the patched protein
 XX CC is expressed and isolating the patched protein free of other proteins.
 XX CC The cell expressing the DNA sequence is also useful for screening
 XX CC candidate compounds for binding affinity to the patched protein, by
 XX CC combining the candidate protein with the cell expressing the DNA sequence
 XX CC where the DNA sequence comprises the entire coding sequence under the
 XX CC transcriptional regulation of the transcriptional initiation region and a
 XX CC transcriptional termination region functional in the cell, expressing the
 XX CC patched protein in the cell and assaying for the binding of the candidate
 XX CC compound to the patched protein. The above cell is useful for screening
 XX CC candidate compounds for agonist activity with the patched protein. The
 XX CC DNA sequence is useful for producing all or portions of the patched
 XX CC protein, as probes for research, diagnosis, binding of hedgehog protein
 XX CC for its isolation and purification and in gene therapy. The DNA sequence
 XX CC is also useful as primers for investigating other species and for
 XX CC isolating genes from various mammalian sources of interest, particularly
 XX CC from humans or from domestic animals. The DNA sequence is further useful
 XX CC for preparing transgenic laboratory animals and to knock out the PTC
 XX CC protein in the embryonic stem cells, so as to produce hosts with single
 XX CC functional patched gene. The present sequence represents the amino acid
 XX CC sequence of the mouse patched gene PTC product
 XX SQ Sequence 1434 AA;
 Query Match 1.2%; Score 15; DB 7; Length 1434;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 451 FNAATTQVLPLALG 465
 Db 481 FNAATTQVLPLALG 495
 RESULT 19
 ADE94215
 ID ADE94215 standard; protein; 1434 AA.

XX AC ADE94215;
 XX DT 12-FEB-2004 (first entry)
 XX DE Murine ptc polypeptide.
 XX DE Murine ptc polypeptide.
 XX KW Mouse; patched gene; ptc; developmental abnormality;
 XX KW proliferative disorder; tumour; oncogenic patched mutation;
 XX KW patched-associated phenotype; basal cell nevus syndrome; BCNS; carcinoma;
 XX KW meningioma; fibroma; cancer.
 XX OS Mus sp.
 XX PN US6551782-B1.
 XX PD 22-APR-2003.
 XX PF 28-NOV-2000; 2000US-00724631.
 XX PR 07-OCT-1994; 94US-00319745.
 XX PR 06-OCT-1995; 95US-00540406.
 XX PR 31-MAY-1996; 96US-00656055.
 XX PR 22-AUG-1997; 97US-00918658.
 XX PA (STRD) UNIV STANFORD.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Scott MP, Goodrich LV, Johnson RL, Epstein E;
 XX DR WPI; 2003-615308/58.
 XX DR N-PSDB; ADE94214.
 XX PT Assay for phenotyping patched status of cell in mammalian (preferably
 XX PT human) cell sample, involves detecting presence or absence of aberrant
 XX PT modification or mutation of a patched gene, and mis-expression of patched
 XX PT gene.
 XX PS Disclosure; SEQ ID NO 10; 57pp; English.
 XX CC The invention relates to an assay for phenotyping the patched status of a
 XX CC cell, involving detecting in vitro, in a sample of mammalian cells, the
 XX CC presence or absence of a genetic lesion in a patched gene (ptc)
 XX CC characterised by at least one of an aberrant modification or mutation of
 XX CC a patched gene or mis-expression of the patched gene. The invention also
 XX CC relates to a method for diagnosing a genetic predisposition of an animal
 XX CC to a developmental abnormality or a proliferative disorder, where the
 XX CC developmental abnormality or proliferative disorder correlates with
 XX CC aberrant expression or activity of a patched gene or gene product.
 XX CC involving detecting in vitro the presence of a predisposing mutation in a
 XX CC patched gene in cells of the animal. Characterising the phenotype of a
 XX CC tumour, involves detecting the presence of an oncogenic patched mutation
 XX CC in cells of the tumour, where the presence of the oncogenic mutation
 XX CC indicates that the tumour has a patched-associated phenotype. The assay
 XX CC is useful for phenotyping the patched status of the cell in a mammalian
 XX CC cell sample obtained from a human patient. The disorders that can be
 XX CC detected include basal cell nevus syndrome (BCNS), carcinomas,
 XX CC meningiomas and fibromas. This sequence represents a murine ptc
 XX CC polypeptide of the invention.
 XX SQ Sequence 1434 AA;
 Query Match 1.2%; Score 15; DB 7; Length 1434;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 451 FNAATTQVLPLALG 465
 Db 481 FNAATTQVLPLALG 495
 RESULT 20
 ADH62722

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ID ADH62722 standard; protein; 1434 AA.
XX AC
XX ADH62722;
XX DT
XX 25-MAR-2004 (first entry)
XX DE
XX Mouse patched (mptc) protein.
XX KW
XX PTC; patched; embryonic development; cellular regulation;
XX signal transduction; mouse.
XX OS
XX Mus sp.
XX PN
XX US2003148388-A1.
XX PD
XX 07-AUG-2003.
XX PF
XX 03-JAN-2001; 2001US-00754032.
XX PR
XX 07-OCT-1994; 94US-00319745.
XX 06-OCT-1995; 95US-00540406.
XX PR
XX 20-OCT-1997; 97US-00354668.
XX PA
XX (STRD ) UNIV STANFORD.
XX PI
XX Scott MP, Goodrich LV, Johnson RL;
XX WPI; 2003-897566/82.
XX N-PSDB; ADH62721.
XX
XX New DNA sequences encoding patched protein from organisms including human
XX and mouse are used to elucidate embryonic development and cellular
XX regulation associated with patched signal transduction and identify
XX patched ligands.
XX PS
XX Disclosure; SEQ ID NO 10; 40pp; English.
XX
XX The present invention relates to a DNA sequence encoding a patched (PTC)
XX gene. The invention is used to elucidate embryonic development, cellular
XX regulation associated with signal transduction by the patched gene,
XX identify agonists and antagonists of that signal transduction, identify
XX and isolate ligands of patched protein and assay for levels of
XX transcription of the patched gene. The present sequence is the mouse
XX patched protein.
XX SQ
XX Sequence 1434 AA;
XX
XX Query Match 1.2%; Score 15; DB 7; Length 1434;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

RESULT 21
ADE48980
ID ADE48980 standard; protein; 1434 AA.
XX AC
XX ADE48980;
XX DT
XX 29-JAN-2004 (first entry)
XX DE
XX Mouse patched protein (ptc).
XX KW
XX cytosolic; vulnary; gene therapy; phenotyping; patched status;
XX patched gene; genetic predisposition; basal cell nevus syndrome; tumour;
XX carcinoma; meningioma; medulloma; fibroma; cancer; wound healing; aging;
XX mouse; patched gene; ptc.
XX OS
XX Mus sp.
XX

PN US2003186309-A1.
XX
XX 02-OCT-2003.
XX PF
XX 22-APR-2003; 2003US-00421446.
XX XX
XX 07-OCT-1994; 94US-00319745.
XX 06-OCT-1995; 95US-00540406.
XX PR
XX 31-MAY-1996; 96US-00656055.
XX PR
XX 22-AUG-1997; 97US-00918658.
XX PR
XX 28-NOV-2000; 2000US-00724631.
XX PA
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX (REGC ) UNIV CALIFORNIA.
XX PI
XX Scott MP, Goodrich LV, Johnson RL, Epstein E;
XX PF
XX WPI; 2004-041193/04.
XX N-PSDB; ADE48979.
XX XX
XX Phenotyping the patched status of a cell for diagnosing a genetic
XX predisposition for a tumor comprises detecting the presence or absence of
XX a genetic lesion having aberrant modification, mutation or mis-expression
XX of the patched gene.
XX PS
XX Disclosure; SEQ ID NO 10; 60pp; English.
XX
XX The invention describes an assay for phenotyping the patched status of a
XX cell comprising detecting in a sample of mammalian cells the presence or
XX absence of a genetic lesion having aberrant modification or mutation of a
XX patched gene or mis-expression of the patched gene. The assay is useful
XX for diagnosing a genetic predisposition of an animal, e.g. basal cell
XX nevus syndrome, predisposition for developing tumour, i.e. carcinoma,
XX meningioma, medulloma, or fibroma. A genetic construct encoding a patched
XX polypeptide is used to treat an animal having a disorder comprising loss
XX of function of a wild-type patched gene, such as cancer, and can enhance
XX patch function in e.g. wound healing and aging. This sequence is encoded
XX by the mouse patched gene.
XX SQ
XX Sequence 1434 AA;
XX
XX Query Match 1.2%; Score 15; DB 8; Length 1434;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPLALG 465
Db 481 FNAATTQVLPLALG 495

RESULT 22
AAR75375
ID AAR75375 standard; protein; 1447 AA.
XX AC
XX AAR75375;
XX DT
XX 30-JUL-1996 (first entry)
XX DE
XX Human patched protein.
XX KW
XX Patched gene; PTC protein; embryo development; cellular regulation;
XX signal transduction; ligand; antibody; hedgehog protein.
XX OS
XX Homo sapiens.
XX PN
XX WO9611260-A1.
XX XX
XX 18-APR-1996.
XX PD
XX 06-OCT-1995; 95WO-US013233.
XX PF
XX 07-OCT-1994; 94US-00319745.
XX PR
XX

```

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX Scott MP, Goodrich LV, Johnson RL;
 XX WPI; 1996-209842/21.
 DR N-PSDB; AAT14220.
 XX
 PT DNA encoding patched protein other than Drosophila patched protein - used
 PT to produce antibodies which detect or inhibit patched protein ligand
 PT signal transduction in cells.
 XX
 XX Example; Page 56-61; 70pp; English.
 XX
 CC Human patched protein (PTC) (AA75375) was identified as the product of a
 CC cDNA clone (AAT14220) derived from human lung. It has 96% identity and
 CC 98% similarity to mouse PTC. PTC protein has been proposed as a receptor
 CC for hedgehog protein on the basis of genetic experiments in flies. Human
 CC PTC protein can be obtd. in large amounts by expression of the cDNA clone
 CC in transformed host cells. It can be used to screen for agonists and
 CC antagonists, to isolate its ligand, partic. Sonic hedgehog, to assay for
 CC the transcription of ptc mRNA and to raise antibodies
 XX
 SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 2; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 495 FNAATTQVLPLALG 509

RESULT 23

AAW52200
 ID AAW52200 standard; protein; 1447 AA.
 XX
 AC AAW52200;
 XX
 DT 25-JUN-1998 (first entry)
 XX
 DE Human patched (ptc) protein.
 XX
 KW Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter;
 KW wound healing; ageing; human.
 XX
 OS Homo sapiens.
 XX
 PN W09745541-A2.
 XX
 PD 04-DEC-1997.
 XX
 PF 02-JUN-1997; 97WO-US009553.
 XX
 PR 31-MAY-1996; 96US-00656055.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (REGC) UNIV CALIFORNIA.
 XX
 XX Scott MP, Goodrich LV, Johnson RL, Epstein E, Oro A;
 XX
 DR WPI; 1998-032648/03.
 DR N-PSDB; AAV21590.
 XX
 PT Patched protein other than Drosophila melanogaster patched protein - used
 PT for characterising the phenotype of a tumour.
 XX
 XX Claim 4; Page 76-80; 86pp; English.
 XX
 CC This is a human patched (ptc) protein. The encoding DNA can be used to
 CC construct an expression cassette comprising an altered patch or hedgehog
 CC gene. The expression cassette comprises a nucleic acid encoding a patched
 CC protein other than a Drosophila melanogaster patched protein, or fragment

CC of at least 12 nucleotides in length, as other than an intact chromosome
 CC under transcriptional control of a transcriptional initiation region, and
 CC a transcriptional termination region, both functional in an expression
 CC host. A genetically engineered mammalian cell comprising this expression
 CC cassette as an extrachromosomal element or integrated into the genome of
 CC the cell can be predisposed to develop basal cell carcinoma as a result
 CC of the transfection. By analysing DNA, functional analysis of patched
 CC protein function, or by detecting antibody binding to abnormal patched
 CC protein, a genetic predisposition to developmental abnormalities and
 CC cancer can be diagnosed. This analysis can also be used for
 CC characterising the phenotype of a tumour, particularly a carcinoma,
 CC especially a basal cell carcinoma. The methods can also be used for
 CC characterising transitional cell carcinoma of the bladder, meningiomas
 CC medulloblastomas, etc. The modified cells comprising the expression
 CC cassette can be used to determine the role of different exons of the
 CC patched gene in oncogenesis, signal transduction, etc. Transgenic animal
 CC models created from these cells can be used as animal models for
 CC carcinomas of the skin. The patched protein of mosquito, butterfly or
 CC beetle or alternatively, a mammalian patched protein of human or mouse
 CC can be used to identify ligands or substrates that bind to, modulate, or
 CC mimic the action of patched gene. These agents could be used as tumour
 CC suppressors, cell adhesion promoters (e.g. in wound healing and ageing)
 XX
 SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 2; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 495 FNAATTQVLPLALG 509

RESULT 24

AAW72969
 ID AAW72969 standard; protein; 1447 AA.
 XX
 AC AAW72969;
 XX
 DT 26-JAN-1999 (first entry)
 XX
 DE Human patched protein.
 XX
 KW Human; patched gene; diagnosis; treatment; developmental disorder;
 KW cancer; healing; injured tissue; ptc; spina bifida; Wnt-1 oncogene;
 KW sperm production; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5837538-A.
 XX
 PD 17-NOV-1998.
 XX
 PF 06-OCT-1995; 95US-00540406.
 XX
 PR 07-OCT-1994; 94US-00319745.
 XX
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Scott MP, Goodrich LV, Johnson RL;
 XX
 DR WPI; 1999-023461/02.
 DR N-PSDB; AAV64093.
 XX
 PT Nucleic acid encoding vertebrate patched protein and related
 PT transformants - used to express poly:peptide(s), useful for diagnosis and
 PT treatment of developmental disorders or cancer, and in healing of injured
 PT tissue.
 XX
 XX Claim 23; Col 63-70; 38pp; English.
 XX
 CC The present sequence represents the human patched (ptc) protein. Cells

CC containing and expressing the ptc gene are used for the recombinant
 CC production of the protein. These in turn are useful: (i) for generating
 CC antibodies (Ab); and (ii) to screen for specific-binding ligands
 CC (potential therapeutic agonists and antagonists). The ptc gene, or its
 CC fragments, are used to isolate related sequences from other mammals; to
 CC identify mutations (particularly those associated with genetic diseases
 CC such as spina bifida and other developmental disorders); to monitor
 CC expression levels in testis (to determine relationship with sperm
 CC production) and to isolate 5'-non-coding sequences (used to study
 CC embryonic development and to provide regulated expression of proteins).
 CC The complete gene can be used in gene therapy, including expression of
 CC antisense molecules, and to generate transgenic animals for studies of
 CC embryonic development. Ab are used diagnostically to determine the ptc
 CC protein on cell surfaces and as competitive inhibitors of signal
 CC transduction through the ptc ligand. Cells that have been engineered to
 CC express the ptc protein can be used to promote regrowth and healing of
 CC damaged tissue (e.g. growth of new teeth) and regulation of the ptc
 CC protein expression may be useful in cancer treatment (it may control the
 CC Wnt-1 oncogene)
 XX
 SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 2; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 495 FNAATTQVLPLALG 509

RESULT 25
 AAB67163
 ID AAB67163 standard; protein; 1447 AA.
 XX
 AC AAB67163;
 XX
 DT 12-APR-2001 (first entry)
 XX
 DE Human patched protein.
 XX
 KW Human; patched; PTC; segment polarity; limb patterning; development;
 KW hedgehog; antibody; mouse.
 XX
 OS Homo sapiens.
 XX
 PN US6172200-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 20-OCT-1997; 97US-00954668.
 XX
 PR 07-OCT-1994; 94US-00319745.
 PR 06-OCT-1995; 95US-00540406.
 XX
 PA (STRD) UNIV LELAND S STANFORD.
 XX
 PI Scott MP, Goodrich LV, Johnson RL;
 XX
 DR WPI; 2001-136884/14.
 DR N-PSDB; AAF32185.
 XX
 PT Novel monoclonal antibody useful in diagnostic assays for detection of
 PT presence of protein on surface of cells specifically binds to naturally
 PT occurring patched protein, other than Drosophila patched protein.
 XX
 PS Disclosure; Col 61-70; 39pp; English.
 XX
 CC The present invention provides a monoclonal antibody which specifically
 CC binds to a patched protein (PTC) other than that from Drosophila. Also
 CC given are the protein and coding sequences of patched from the beetle,
 CC mouse, butterfly, fruit fly, mosquito and human. Patched is a segment
 CC polarity gene involved in limb patterning. The sequences can be used to

CC study development and to isolate the patched ligand, hedgehog. In
 CC addition, antibodies can be used to detect the PTC protein on cell
 CC surfaces or to inhibit the transduction of signal by the PTC ligand by
 CC competing for its binding site
 XX
 SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 4; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 495 FNAATTQVLPLALG 509

RESULT 26
 AAE19830
 ID AAE19830 standard; protein; 1447 AA.
 XX
 AC AAE19830;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human patched (Ptc) protein.
 XX
 KW Human; patched; Ptc; cell proliferation; differentiation; therapy;
 KW cytostatic; testicular cancer; hedgehog protein signalling.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT Domain 100..119
 FT /label= TM1
 FT /note= "Transmembrane domain"
 FT Domain 438..458
 FT /label= TM2
 FT /note= "Transmembrane domain"
 FT Domain 471..493
 FT /label= TM3
 FT /note= "Transmembrane domain"
 FT Domain 502..521
 FT /label= TM4
 FT /note= "Transmembrane domain"
 FT Domain 548..570
 FT /label= TM5
 FT /note= "Transmembrane domain"
 FT Domain 578..599
 FT /label= TM6
 FT /note= "Transmembrane domain"
 FT Domain 751..769
 FT /label= TM7
 FT /note= "Transmembrane domain"
 FT Domain 1028..1048
 FT /label= TM8
 FT /note= "Transmembrane domain"
 FT Domain 1052..1074
 FT /label= TM9
 FT /note= "Transmembrane domain"
 FT Domain 1078..1097
 FT /label= TM10
 FT /note= "Transmembrane domain"
 FT Domain 1122..1141
 FT /label= TM11
 FT /note= "Transmembrane domain"
 FT Domain 1155..1178
 FT /label= TM12
 FT /note= "Transmembrane domain"
 XX
 PN US6348575-B1.
 XX
 PD 19-FEB-2002.
 XX

PF 15-APR-1999; 99US-00293505.
 XX
 PR 15-APR-1998; 98US-0081884P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI De Sauvage F, Carpenter DA;
 XX
 DR WPI; 2002-215260/27.
 XX
 XX Native human patched-2 polypeptide for treating disorders caused by
 PT Hedgehog protein signaling such as testicular cancer, and for screening
 PT cDNA libraries.
 XX
 PS Example 1; Fig 3; 82pp; English.
 XX
 CC The invention relates to an isolated sequence comprising a native human
 CC patched-2 (Ptc-2) polypeptide. The invention also relates to signalling
 CC and mediator molecules in the hedgehog (Hh) cascade which are involved in
 CC cell proliferation and differentiation. The isolated sequence is useful
 CC for the treatment of disorders which are linked to Hedgehog, especially
 CC Desert hedgehog expression, such as testicular cancer. It may also be
 CC used as a hybridisation probe in a cDNA library to isolate Ptc-2 or its
 CC homologues, and to diagnose whether a disorder is driven by Ptc-2 or
 CC Hedgehog protein signalling. The present sequence is human patched (Ptc)
 CC protein. Note: The sequence shown as SEQ ID NO: 4 in sequence listing of
 CC the specification is a fragment of the sequence shown as SEQ ID NO: 4 in
 CC fig 3 of the specification
 XX
 SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 5; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 DB 495 FNAATTQVLPLALG 509

RESULT 27
 ABJ10931
 ID ABJ10931 standard; protein; 1447 AA.
 XX
 AC ABJ10931;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE TRC8 related human patched protein SEQ ID No 5.
 XX
 KW TRC8; Translocation in Renal cancer from Chromosome 8; fused DNA; 3,2;
 KW FHIT/TRC8 fusion DNA; sporadic renal cell carcinoma; TRC8/FHIT; TRC8FHIT;
 KW human chromosomal translocation.
 XX
 OS Homo sapiens.
 XX
 PN US2002106656-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 02-JUL-2001; 2001US-00898533.
 XX
 PR 12-MAR-1998; 98US-0077723P.
 PR 12-MAR-1999; 99US-00268140.
 XX
 PA (GEMM/) GEMMILL R M.
 PA (DRAB/) DRABKIN H A.
 XX
 PI Gemmill RM, Drabkin HA;
 XX
 DR WPI; 2002-712395/77.
 XX
 PT Novel Translocation in Renal cancer from Chromosome 8 genes, useful for

PT detection of tumors, comprises rearrangements in the t(3;8) (p14.2;q24.1)
 PT chromosomal translocation which occurs in renal and thyroid carcinomas.
 XX
 PS Disclosure; Fig 2D; 49pp; English.
 XX
 CC The invention relates to an isolated TRC8 (Translocation in Renal cancer
 CC from Chromosome 8) nucleic acid molecule, encoding a polypeptide
 CC comprising a sequence of 664 amino acids, fully defined in the
 CC specification and comprising a sequence located in the 5' flanking region
 CC to the coding region of TRC8 and a sequence which occurs in certain
 CC sporadic renal cell carcinomas. The methods are useful for detecting the
 CC presence of the TRC8 gene in a biological sample, detecting alterations
 CC to the gene, such as a 3;2 human chromosomal translocation, and fused DNA
 CC containing the fused site of TRC8/FHIT. A nucleic acid probe is useful
 CC for detecting the 3;8 human chromosomal translocation, by contacting the
 CC nucleic acid probe with a biological sample to be tested, and determining
 CC whether the nucleic acid probe specifically hybridises to the TRC8FHIT or
 CC FHIT/TRC8 fusion DNA. This sequence represents a TRC8 related protein of
 CC the invention
 XX
 SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 5; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 DB 495 FNAATTQVLPLALG 509

RESULT 28
 AAG79571
 ID AAG79571 standard; protein; 1447 AA.
 XX
 AC AAG79571;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human patched protein.
 XX
 KW Patched; ptc; basal cell nevus syndrome; BCNS; wound healing;
 KW developmental disorder; spina bifida; craniofacial abnormality;
 KW basal cell carcinoma; skin; brain tumour; transgenic; mouse;
 KW proliferation; oncogenesis; signal transduction; cancer; aging.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 113
 FT /note= "Encoded by CCG"
 FT Misc-difference 413
 FT /note= "Encoded by GAG"
 FT Misc-difference 864
 FT /note= "Encoded by GAA"
 XX
 PN US6429354-B1.
 XX
 PD 06-AUG-2002.
 XX
 PF 22-AUG-1997; 97US-00918658.
 XX
 PR 07-OCT-1994; 94US-00319745.
 PR 06-OCT-1995; 95US-00540406.
 PR 31-MAY-1996; 96US-00656055.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Scott MP, Goodrich LV, Johnson RL, Epstein E;
 XX
 DR WPI; 2002-722086/78.
 DR N-PSDB; ABA00374.

XX Transgenic mouse, useful for cancer drug screening, comprises disruption
 PT of allele of patched locus which predisposes the mouse to develop a
 PT proliferative disorder.

XX Disclosure; Col 85-92; 58pp; English.

XX This sequence shows human patched (ptc) protein. Human patched gene has
 CC been mapped to human chromosome band 9q22.3 and lies between two
 CC polymorphic markers D9S196 and D9S287. Mutations in the patched gene are
 CC characteristic in basal cell nevus syndrome (BCNS), an inherited disorder
 CC with an increased risk of developmental disorders such as spina bifida
 CC and craniofacial abnormalities, basal cell carcinoma of the skin and
 CC brain tumours. The human and mouse ptc sequences show 86% homology. The
 CC transgenic mouse of the invention has a genome comprising a disruption of
 CC at least one allele of a patched locus, where the disruption predisposes
 CC the mouse to develop a proliferative disorder. The transgenic mouse is
 CC useful for studying patched function and regulation, for e.g. a series of
 CC small deletions and/or substitutions made in the patched gene, to
 CC determine the role of different exons in oncogenesis, signal
 CC transduction, etc; and for drug screening which is useful for treating
 CC cancer or developmental abnormalities attributed to a defect in patched
 CC function such as wound healing and aging

XX SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 5; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 495 FNAATTQVLPLALG 509

RESULT 29

ABU62275
 ID ABU62275 standard; protein; 1447 AA.

AC ABU62275;

XX 25-AUG-2003 (first entry)

DT Human patched gene PTC product.

DE Human; patched gene; PTC; hedgehog protein; gene therapy.

KW Homo sapiens.

XX US2003032085-A1.

PN 13-FEB-2003.

XX 20-OCT-1997; 97US-00954701.

XX 07-OCT-1994; 94US-00319745.

PR 06-OCT-1995; 95US-00540406.

XX (SCOT/) SCOTT M P.

PA (GOOD/) GOODRICH L V.

PA (JOHN/) JOHNSON R L.

XX Scott MP, Goodrich LV, Johnson RL;

XX WPI; 2003-492065/46.

XX New DNA sequence other than present in a chromosome encoding patched gene
 PT other than Drosophila patched gene, useful for preparing transgenic
 PT laboratory animals and to knock out patched protein in embryonic stem
 PT cells.

XX Disclosure; Page 8-10; 40pp; English.

CC The invention relates to a DNA sequence other than present in chromosome
 CC encoding a patched (ptc) gene other than Drosophila patched gene. A cell
 CC expressing the DNA sequence is useful for producing patched protein, by
 CC growing the cell expressing the DNA sequence, where the patched protein
 CC is expressed and isolating the patched protein free of other proteins.
 CC The cell expressing the DNA sequence is also useful for screening
 CC candidate compounds for binding affinity to the patched protein, by
 CC combining the candidate protein with the cell expressing the DNA sequence
 CC where the DNA sequence comprises the entire coding sequence under the
 CC transcriptional regulation of the transcriptional initiation region and a
 CC transcriptional termination region functional in the cell, expressing the
 CC patched protein in the cell and assaying for the binding of the candidate
 CC compound to the patched protein. The above cell is useful for screening
 CC candidate compounds for agonist activity with the patched protein. The
 CC DNA sequence is useful for producing all or portions of the patched
 CC protein, as probes for research, diagnosis, binding of hedgehog protein
 CC for its isolation and purification and in gene therapy. The DNA sequence
 CC is also useful as primers for investigating other species and for
 CC isolating genes from various mammalian sources of interest, particularly
 CC from humans or from domestic animals. The DNA sequence is further useful
 CC for preparing transgenic laboratory animals and to knock out the PTC
 CC protein in the embryonic stem cells, so as to produce hosts with single
 CC functional patched gene. The present sequence represents the amino acid
 CC sequence of the human patched gene PTC product
 XX

SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 7; Length 1447;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALG 465
 |||||
 Db 495 FNAATTQVLPLALG 509

RESULT 30

ADD46678

ID ADD46678 standard; protein; 1447 AA.

XX ADD46678;

XX 02-DEC-2004 (revised)

DT 29-JAN-2004 (first entry)

XX Human Protein NP_000255, SEQ ID NO 12363.

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

OS Unidentified.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; NP_000255.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Example 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1447 AA;

Query Match 1.2%; Score 15; DB 7; Length 1447;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLFPFLALG 465

|||||||

Db 495 FNAATTQVLFPFLALG 509

Search completed: June 16, 2005, 08:04:39
Job time : 181 secs

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OM protein - protein search, using sw model

Run on: June 16, 2005, 07:56:46 ; Search time 51 Seconds
(without alignments)
2269.584 Million cell updates/sec

Title: US-09-990-046A-2

Perfect score: 1203

Sequence: 1 MTRSPPLRELPPSYTPPTA.....SPAATSSGNLSRGPATG 1203

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

PIR-79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	7.8	1182	2 T13952	membrane protein p
2	20	1.7	1220	2 T18291	patched protein -
3	15	1.2	1434	2 T30172	transmembrane prot
4	15	1.2	1442	2 T18538	patched protein -
5	11	0.9	714	2 T16126	hypothetical prote
6	11	0.9	1405	2 T27969	hypothetical prote
7	9	0.7	249	2 E95292	probable ABC trans
8	9	0.7	308	2 AC2123	permease protein o
9	9	0.7	1081	2 B81303	probable membrane
10	9	0.7	1299	1 S06119	membrane protein p
11	8	0.7	75	2 C71370	hypothetical prote
12	8	0.7	99	2 B81051	L-lactate permease
13	8	0.7	99	2 D81825	probable integral
14	8	0.7	196	2 A30327	corticosteroid pre
15	8	0.7	211	2 E72609	hypothetical prote
16	8	0.7	232	2 T44456	arginine/ornithine
17	8	0.7	262	2 G83812	chitin-binding pro
18	8	0.7	286	2 D84590	probable inhibiti
19	8	0.7	320	2 E71139	hypothetical prote
20	8	0.7	340	2 T19538	hypothetical prote
21	8	0.7	357	2 D72589	hypothetical prote
22	8	0.7	377	2 AD1911	hypothetical prote
23	8	0.7	379	2 G75357	diaminopimelate de
24	8	0.7	388	2 T14362	glutamate synthase
25	8	0.7	422	2 T09120	basic leucine zipp
26	8	0.7	440	2 F70792	hypothetical prote
27	8	0.7	444	2 C90704	Rhs core protein {
28	8	0.7	444	2 G85554	Rhs core protein {
29	8	0.7	454	2 T18765	hypothetical prote

hypothetical prote
nif-specific regul
cytochrome P450 CY
islet cell antigen
serine transducer
methyl-accepting c
vesicle transport
aspartate kinase (c
penicillin-binding
hypothetical prote
retrovirus-related
pol polyprotein -
pol polyprotein -
isoleucyl-tRNA syn
protein-tyrosine-p
hypothetical prote
hypothetical prote
protein-tyrosine-p
probable receptor-
PTP 35 protein - m
hypothetical prote
probable polyketid
adhesin P1, group
adhesin P1, group
phosphorylase b -
hypothetical prote
hypothetical prote
outer envelope mem
probable membrane
hypothetical prote
protein F24O1.6 [i
SEC-independent pr
hypothetical prote
chlorophyll a/b-bi
chlorophyll a/b-bi
hypothetical prote
cobalt transport p
hypothetical prote
E7 protein - human
NADH2 dehydrogenas
hypothetical prote
GTP-binding protei
hypothetical prote
hypothetical prote
hypothetical prote
rubredoxin import
conserved hypothet
hypothetical prote
colipase precursor
hypothetical prote
probable membrane
hypothetical prote
hypothetical prote
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
Ig kappa chain V r
probable pol prote
Ig kappa chain - h
Ig kappa chain - h
Ig kappa chain - h
probable glycine-z
Ig kappa chain - h
diacylglycerol kin
Ig kappa chain V-J
Ig kappa chain - h
Ig kappa chain - h
Ig kappa chain V r
Ig kappa chain pre

ALIGNMENTS

```
RESULT 1
T13952
membrane protein ptch2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13952
R;Motoyama, J.; Takabatake, T.; Takashima, K.; Hui, C.
Nature Genet. 18, 104-106, 1998
A>Title: Ptch2, a second mouse Patched gene is co-expressed with Sonic hedgehog.
A:Reference number: Z17830; MUID:98122566; PMID:9462734
A:Accession: T13952
A:Molecule type: mRNA
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-1182 <MOT>
A:Cross-references: UNIPROT:O35595; EMBL:AB010833; PIDN:BAA24691.1
A:Experimental source: strain BALB/cCrSlc
C:Genetics:
C:Superfamily: Drosophila membrane protein patched
C:Keywords: transmembrane protein

Query Match      7.8%; Score 94; DB 2; Length 1182;
Best Local Similarity 100.0%; Pred. No. 1.le-85;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      693 FGALLGSLYGATLVQDGLALTVDVPRGTEKHEAFSLAQRLYFSLYEVALVTQGGFDVAHS 752
Db      693 FGALLGSLYGATLVQDGLALTVDVPRGTEKHEAFSLAQRLYFSLYEVALVTQGGFDVAHS 752

Qy      753 QRALFDLHQRFSSLKAVLPPPATQAPRTWLHYR 786
Db      753 QRALFDLHQRFSSLKAVLPPPATQAPRTWLHYR 786

RESULT 2
T18291
patched protein - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18291
R;Concordet, J.P.; Lewis, K.E.; Moore, J.W.; Goodrich, L.V.; Johnson, R.L.; Scott, M.P.;
Development 122, 2835-2846, 1996
A>Title: Spatial regulation of a zebrafish patched homologue reflects the roles of sonic
A:Reference number: Z18860; MUID:96379744; PMID:8787757
A:Accession: T18291
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1220 <CON>
A:Cross-references: UNIPROT:Q98864; EMBL:X98883; PIDN:CAA67386.1
C:Genetics:
A:Gene: ptcl
C:Superfamily: Drosophila membrane protein patched

Query Match      1.7%; Score 20; DB 2; Length 1220;
Best Local Similarity 100.0%; Pred. No. 6.le-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      400 GGYLLMLAYACVTMLRWDC 419
Db      427 GGYLLMLAYACVTMLRWDC 446

RESULT 3
T30172
transmembrane protein patched - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30172
R;Goodrich, L.V.; Johnson, R.L.; Milenkovic, L.; McMahon, J.A.; Scott, M.P.
Genes Dev. 10, 301-312, 1996
```

```
A>Title: Conservation of the hedgehog/patched signaling pathway from flies to mice: indi
A:Reference number: Z20752; MUID:96176226; PMID:8595881
A:Accession: T30172
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1434 <GOO>
A:Cross-references: UNIPROT:Q61115; EMBL:U46155; NID:g1181884; PID:g1181885; PIDN:AAC98
A:Experimental source: clone M2, M9
C:Superfamily: Drosophila membrane protein patched

Query Match      1.2%; Score 15; DB 2; Length 1434;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      451 FNAATTQVLFFLALG 465
Db      481 FNAATTQVLFFLALG 495

RESULT 4
T18538
patched protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18538
R;Marigo, V.; Scott, M.P.; Johnson, R.L.; Goodrich, L.V.; Tabin, C.
Development 122, 1225-1233, 1996
A>Title: Conservation in hedgehog signaling: induction of a chicken patched homolog by
A:Reference number: Z18958; MUID:96205046; PMID:8620849
A:Accession: T18538
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1442 <MAR>
A:Cross-references: UNIPROT:Q90693; EMBL:U40074; NID:g1335850; PID:g1335851; PIDN:AAC55
C:Genetics:
A:Gene: PTC
C:Superfamily: Drosophila membrane protein patched
C:Keywords: transmembrane protein

Query Match      1.2%; Score 15; DB 2; Length 1442;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      451 FNAATTQVLFFLALG 465
Db      495 FNAATTQVLFFLALG 509

RESULT 5
T16126
hypothetical protein F21H12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16126
R;Favello, T.
submitted to the EMBL Data Library, July 1995
A>Description: The sequence of C. elegans cosmid F21H12.
A:Reference number: Z18464
A:Accession: T16126
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-714 <FAV>
A:Cross-references: UNIPROT:Q09540; EMBL:U23176; NID:g726404; PID:g726409; PIDN:AAC4671
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F21H12.4
A:Introns: 25/1; 334/2; 430/2; 543/3

Query Match      0.9%; Score 11; DB 2; Length 714;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1026 VGIGVEFTVHV 1036
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Db 660 VGIGVEFTVHV 670
|||||

RESULT 6
T27969
hypothetical protein ZK675.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27969
R;Sims, M.
submitted to the EMBL Data Library, November 1994
A;Reference number: Z20448
A;Accession: T27969
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-1405 <NLS>
A;Cross-references: UNIPROT:Q09614; EMBL:Z46812; PIDN:CAA86843.1; GSPDB:GN00020; CESP:ZK675.1
A;Experimental source: clone ZK675
C;Genetics:
A;Gene: CESP:ZK675.1
A;Map position: 2
A;Introns: 31/1; 59/3; 100/3; 244/2; 485/1; 950/2; 1298/2; 1335/3
C;Superfamily: Drosophila membrane protein patched

Query Match 0.9%; Score 11; DB 2; Length 1405;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1026 VGIGVEFTVHV 1036
|||||

Db 1242 VGIGVEFTVHV 1252

RESULT 7
E95292
probable ABC transporter, permease SMA0469 [imported] - *Sinorhizobium meliloti* (strain 1021)
C;Species: *Sinorhizobium meliloti*
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95292
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowsby, J.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti* ABC transporter
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: E95292
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <KUR>
A;Cross-references: UNIPROT:Q930F3; GB:AR006469; PIDN:AAK64903.1; PID:g14523323; GSPDB:G14523323
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Pel, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, J.; Heubalt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.
A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Contents: annotation
C;Genetics:
A;Gene: SMA0469

C;Superfamily: oligopeptide permease protein oppB
Query Match 0.7%; Score 9; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1066 AISTLLGLL 1074
|||||

Db 67 AISTLLGLL 75

RESULT 8
AC2123

permease protein of branched-chain amino acid ABC transporter alr2538 [imported] - *Nostoc sp.* PCC 7120
C;Species: *Nostoc sp.* PCC 7120
A;Note: *Nostoc sp.* strain PCC 7120 is a synonym of *Anabaena sp.* strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC2123
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriouchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, D. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing *Cyanobacterium* Anabaena PCC 7120
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2123
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <KUR>
A;Cross-references: UNIPROT:Q8YU23; GB:BA000019; PIDN:BA874237.1; PID:g17131630; GSPDB:BA874237.1
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr2538
C;Superfamily: leucine transport protein livH

Query Match 0.7%; Score 9; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 694 GALLGLSLY 702
|||||

Db 18 GALLGLSLY 26

RESULT 9
B81303

probable membrane protein Cj1013c [imported] - *Campylobacter jejuni* (strain NCTC 11168)
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81303
R;Kerker, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrer, Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hy A;Reference number: AB1250; MUID:20150912; PMID:10688204
A;Accession: B81303
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1081 <PAR>
A;Cross-references: UNIPROT:Q9PNS7; GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB732
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1013c

Query Match 0.7%; Score 9; DB 2; Length 1081;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 441 LGLCALLGI 449
|||||

Db 915 LGLCALLGI 923

RESULT 10
S06119

membrane protein patched - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: S06119; A33468
R;Nakano, Y.; Guerrero, I.; Hidalgo, A.; Taylor, A.; Whittle, J.R.S.; Ingham, P.W. Nature 341, 508-513, 1989
A;Title: A protein with several possible membrane-spanning domains encoded by the *Drosophila* patched gene
A;Reference number: S06119; MUID:90015164; PMID:2797178
A;Accession: S06119
A;Status: not compared with conceptual translation

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A;Molecule type: DNA
A;Residues: 1-1299 <NAK>
A;Cross-references: UNIPROT:P18502; GB:X17558; NID:G8389; PIDN:CAA35591.1; PID:G8390
R;Hooper, J.E.; Scott, M.P.
Cell 59, 751-765, 1989
A;Title: The Drosophila patched gene encodes a putative membrane protein required for se
A;Reference number: A33468; MUID:90058658; PMID:2582494
A;Accession: A33468
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-110, 'R', '112-273, 'G', '275-331, 'R', '333-635, 'P', '637-861, 'DVF', '878, 'Y', '880-1299
A;Cross-references: GB:M28418; GB:M28999; NID:G552097; PID:G552099
C;Genetics:
A;Gene: FlyBase:ptc
A;Cross-references: FlyBase:FBgn0003892
A;Map position: 2 4D3-D4
C;Superfamily: Drosophila membrane protein patched
C;Keywords: glycoprotein; transmembrane protein
F;74-92/Domain: transmembrane #status predicted <TM01>
F;427-448/Domain: transmembrane #status predicted <TM02>
F;456-503/Domain: transmembrane #status predicted <TM03>
F;529-555/Domain: transmembrane #status predicted <TM04>
F;557-585/Domain: transmembrane #status predicted <TM05>
F;677-699/Domain: transmembrane #status predicted <TM06>
F;967-1017/Domain: transmembrane #status predicted <TM07>
F;1019-1047/Domain: transmembrane #status predicted <TM08>
F;1061-1086/Domain: transmembrane #status predicted <TM09>
F;1093-1121/Domain: transmembrane #status predicted <TM10>
F;142,298,335,388,807,861,1194,1271/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 0.7%; Score 9; DB 1; Length 1299;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 TPLDCFWEG 195
Db 207 TPLDCFWEG 215
|||||||

RESULT 11
C71370
hypothetical protein TP0059 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: C71370
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: C71370
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-75 <COL>
A;Cross-references: UNIPROT:O83098; GB:AE001191; GB:AE000520; NID:G3322316; PIDN:AAC6506
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0059

Query Match 0.7%; Score 8; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 PFASLEGF 234
Db 41 PFASLEGF 48
|||||||

RESULT 12
B81051
L-lactate permease-related protein NMB1712 [imported] - Neisseria meningitidis (strain M
C;Species: Neisseria meningitidis
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81051
R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
R;Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <TET>
A;Cross-references: UNIPROT:Q9JY69; GB:AE002521; GB:AE002098; NID:G726962; PIDN:AAE420
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1712

Query Match 0.7%; Score 8; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1088 FFAALTIVL 1095
Db 53 FFAALTIVL 60
|||||||

RESULT 13
D81825
probable integral membrane protein NMA1966 [imported] - Neisseria meningitidis (strain
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: D81825
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
r; Holtroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81825
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <PAR>
A;Cross-references: UNIPROT:Q9JY54; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CAB851
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1966

Query Match 0.7%; Score 8; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1088 FFAALTIVL 1095
Db 53 FFAALTIVL 60
|||||||

RESULT 14
A30327
corticolliberin precursor - human
N;Alternate names: corticotropin-releasing factor
N;Contents: corticolliberin
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: A30327; A60860; I38106
R;Robinson, B.G.; D'Angio Jr., L.A.; Pasieka, K.B.; Majzoub, J.A.
Mol. Cell. Endocrinol. 61, 175-180, 1989
A;Title: Preprocorticotropin releasing hormone: cDNA sequence and in vitro processing.
A;Reference number: A30327; MUID:89137721; PMID:2783917
A;Accession: A30327
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-196 <ROB>
A;Cross-references: UNIPROT:P06850
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R;Sasaki, A.; Tempst, P.; Liotta, A.S.; Margioris, A.N.; Hood, L.E.; Kent, S.B.H.; Sato, J. Clin. Endocrinol. Metab. 67, 768-773, 1988
 A;Title: Isolation and characterization of a corticotropin-releasing hormone-like peptide
 A;Reference number: A60860; MUID:98331316; PMID:3262120
 A;Accession: A60860
 A;Molecule type: protein
 A;Residues: 154-168, X', 170-186 <SAS>
 R;Shibahara, S.; Morimoto, Y.; Furutani, Y.; Notake, M.; Takahashi, H.; Shimizu, S.; Hori
 EMBO J. 2, 775-779, 1983
 A;Title: Isolation and sequence analysis of the human corticotropin-releasing factor pre
 A;Reference number: I38106; MUID:84057755; PMID:6605851
 A;Accession: I38106
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-196 <RES>
 A;Cross-references: EMBL:V00571; NID:g35355; PIDN:CAA23834.1; PID:g35356
 C;Genetics:
 A;Gene: GDB:CRH
 A;Cross-references: GDB:I19804; OMIM:122560
 A;Map position: 8q13-8q13
 C;Superfamily: corticobexin-endorpholiberin; diuretic hormone homology
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-196/Product: corticobexin #status predicted <MAT>
 F;154-194/Product: corticobexin #status predicted <CLN>
 F;154-193/Domain: diuretic hormone homology <DHH>
 F;194/Modified site: amidated carboxyl end (Ile) (amide in mature form from following gl

Query Match 0.7%; Score 8; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 428 AGVLLVAL 435
 Db 9 AGVLLVAL 16
 |||||

RESULT 15
 E72609
 hypothetical protein APE1339 - Aeropyrum pernix (strain KI)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: E72609
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: E72609
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-211 <KAW>
 A;Cross-references: UNIPROT:Q9YCB7; DBJ:AP000061; NID:95104821; PIDN:BA80331.1; PID:dl
 A;Experimental source: strain KI
 C;Genetics:
 A;Gene: APE1339

Query Match 0.7%; Score 8; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 432 LVALAVAS 439
 Db 13 LVALAVAS 20
 |||||

RESULT 16
 T44456
 arginine/ornithine transport system permease protein actM [imported] - Pseudomonas aeru
 N;Alternate names: membrane protein
 C;Species: Pseudomonas aeruginosa
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T44456; G83534

R;Nishijyo, T.; Park, S.M.; Lu, C.D.; Itoh, Y.; Abdelal, A.T.
 J. Bacteriol. 180, 5559-5566, 1998
 A;Title: Molecular characterization and regulation of an operon encoding a system for
 A;Reference number: Z22777; MUID:99008987; PMID:9791103
 A;Accession: T44456
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-232 <NIS>
 A;Cross-references: UNIPROT:O50183; EMBL:AF012537; NID:g3668593; PIDN:AAC71072.1; PID:g
 A;Experimental source: strain PA01
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: G83534
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-232 <STO>
 A;Cross-references: GB:AE004523; GB:AE004091; NID:g9946783; PIDN:AAG04279.1; GSPDB:GN00
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: actM; PA0890
 C;Superfamily: histidine permease protein M

Query Match 0.7%; Score 8; DB 2; Length 232;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 25 ILAGSLKA 32
 Db 115 ILAGSLKA 122
 |||||

RESULT 17
 G83812
 chitin-binding protein BH1303 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: G83812
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: G83812
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-262 <STO>
 A;Cross-references: UNIPROT:Q9KDB1; GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA05
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH1303
 C;Superfamily: Serratia marcescens 21K chitin-binding protein

Query Match 0.7%; Score 8; DB 2; Length 262;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1071 LGLMLLAG 1078
 Db 20 LGLMLLAG 27
 |||||

RESULT 18
 D84590
 probable prohibitin [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: D84590
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Qy 110 YTSQMLIQ 117
 |||||
 Db 199 YTSQMLIQ 206

RESULT 23

G75357
 diaminopimelate decarboxylase - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: G75357
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: G75357

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-379 <WHI>

A;Cross-references: UNIPROT:Q9RTK2; GB:AE002017; GB:AE000513; NID:G6459527; PIDN:AAF1131

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRI758

A;Map position: 1

C;Superfamily: diaminopimelate decarboxylase

Query Match 0.7%; Score 8; DB 2; Length 379;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 308 GELLRAEA 315

|||||
 Db 72 GELLRAEA 79

RESULT 24

T14362
 glutamate synthase (ferredoxin) (EC 1.4.7.1) - red alga (Cyanidium caldarium) chloroplast
 N;Alternate names: Glutamine 2-oxoglutarate aminotransferase; GOGAT enzyme glsF

C;Species: Chloroplast Cyanidium caldarium

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 12-Jul-2004

C;Accession: T14362

R;Valentin, K.U.

Submitted to the EMBL Data Library, March 1996

A;Description: Ferredoxin GOGAT is plastid-encoded in a unicellular rhodophyte, Cyanidiiu

A;Reference number: Z18012

A;Accession: T14362

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-388 <VAL>

A;Cross-references: EMBL:Z70297; NID:G1240002

C;Genetics:

A;Genome: chloroplast

A;Note: glsF

C;Function:

A;Description: catalyzes reversible conversion of L-glutamate and oxidized ferredoxin to

C;Superfamily: Glutamate synthase, large subunit

C;Keywords: chloroplast; oxidoreductase

Query Match 0.7%; Score 8; DB 2; Length 388;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1022 LVASVGIG 1029

|||||
 Db 26 LVASVGIG 33

RESULT 25

T09120
 basic leucine zipper protein - spinach

C;Species: Spinacia oleracea (spinach)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T09120
 R;Bolle, C.; Lueberstedt, T.; Herranen, M.; Herrmann, R.; Oelmueller, R.
 submitted to the EMBL Data Library, January 1998
 A;Description: Molecular characterization of the spinach G-box binding protein family.

A;Reference number: Z16572

A;Accession: T09120

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-422 <BOL>

A;Cross-references: UNIPROT:O49936; EMBL:AJ223624

C;Genetics:

A;Gene: bZIP

C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology

Query Match 0.7%; Score 8; DB 2; Length 422;

Best Local Similarity 100.0%; Pred. No. 33;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 767 KAVLPPPA 774

|||||
 Db 208 KAVLPPPA 215

RESULT 26

F70792

hypothetical protein Rv3693 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: F70792

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.
 Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: F70792

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-440 <COL>

A;Cross-references: UNIPROT:O69661; GB:AL022121; GB:AL123456; NID:G3261559; PIDN:CAA180

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: Rv3693

Query Match 0.7%; Score 8; DB 2; Length 440;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 431 LLVALAVA 438

|||||
 Db 31 LLVALAVA 38

RESULT 27

C90704

Rhs core protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: C90704

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A;Reference number: A96629; MUID:21156231; PMID:11258796

A;Accession: C90704

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-444 <HAY>

A;Cross-references: UNIPROT:Q8XCR7; GB:BA000007; PIDN:BA834026.1; PID:G13360061; GSPDB:

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:
A;Gene: ECs0603

Query Match 0.7%; Score 8; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 867 DPLGLAAS 874
|||||
Db 290 DPLGLAAS 297

RESULT 28

G85554 Rhs core protein [similarity] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85554
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85554
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-444 <STO>
A;Cross-references: UNIPROT:Q8XCR7; GB:A8005174; NID:g12513445; PIDN:AAG54899.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0702

Query Match 0.7%; Score 8; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 867 DPLGLAAS 874
|||||
Db 290 DPLGLAAS 297

RESULT 29

T18765 hypothetical protein B0491.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18765
R;Sulston, J.
submitted to the EMBL Data Library, June 1995
A;Reference number: Z19019
A;Accession: T18765
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-454 <WTL>
A;Cross-references: UNIPROT:Q17511; EMBL:Z49907; PIDN:CAA90086.1; GSPDB:GN00020; CESP:BO
A;Experimental source: clone B0491
C;Genetics:
A;Gene: CESP:B0491.4
A;Map position: 2
A;Introns: 34/1; 71/3; 98/3; 136/2; 176/2; 286/3; 332/1; 374/3; 419/3

Query Match 0.7%; Score 8; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 LVLFGALL 697
|||||
Db 4 LVLFGALL 11

RESULT 30

D72555 hypothetical protein APE1728 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72555
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72555
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-517 <KAW>
A;Cross-references: UNIPROT:Q9YB69; DDBJ:AP000062; NID:g5105244; PIDN:BA80729.1; PID:Q
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1728

Query Match 0.7%; Score 8; DB 2; Length 517;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 427 LAGVLLVA 434
|||||
Db 12 LAGVLLVA 19

Search completed: June 16, 2005, 08:08:54
Job time : 56 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2005, 07:45:06 ; Search time 194 Seconds
(without alignments)

3175.419 Million cell updates/sec

Title: US-09-990-046A-2

Perfect score: 1203

Sequence: 1 MTRSPPLRELPPSYTPPART.....SPAATSSGNLSRRGPGPATG 1203

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1203	100.0	1211	2	Q6UX14
2	1102	91.6	1203	1	PTC2_HUMAN
3	94	7.8	1182	1	PTC2_MOUSE
4	38	3.2	913	2	Q90XE9
5	20	1.7	1220	1	PTC1_BRARE
6	20	1.7	1413	2	Q9DEF3
7	20	1.7	1422	2	Q6IRA5
8	19	1.6	255	1	PTC2_CYNPY
9	15	1.2	234	2	Q8MKE3
10	15	1.2	608	2	Q9Z2A1
11	15	1.2	651	2	Q6TKP9
12	15	1.2	1239	2	Q9DEF4
13	15	1.2	1243	2	Q9W6T6
14	15	1.2	1418	2	Q98SW6
15	15	1.2	1434	1	PTC1_MOUSE
16	15	1.2	1434	2	Q6U750
17	15	1.2	1442	1	PTC1_CHICK
18	15	1.2	1447	1	PTC1_HUMAN
19	13	1.1	183	2	Q86KG7
20	12	1.0	287	2	Q9DDZ0
21	11	0.9	176	2	Q66PH3
22	11	0.9	257	1	PTC1_CYNPY
23	11	0.9	667	2	Q99540
24	11	0.9	1405	1	PTC1_CABEL
25	10	0.8	345	2	Q6TKP8
26	10	0.8	1243	2	Q69ZL6
27	10	0.8	1331	2	Q6T3U3
28	10	0.8	1332	2	Q6R3Q4
29	10	0.8	1333	2	Q6T3U4
30	10	0.8	1359	2	Q9UHC9
31	10	0.8	1438	2	Q9P2K9

32	0.7	200	1	RECR_CHLCV	Q823d7 chlamydomophi
33	0.7	249	2	Q930F3	Q930f3 rhizobium m
34	0.7	308	2	Q8YU23	Q8yu23 anabaena sp
35	0.7	348	2	Q85DX0	Q85dx0 gonorynchus
36	0.7	408	2	Q6Y4V4	Q6y4v4 xenopus lae
37	0.7	418	2	Q7S082	Q7s082 neurospora
38	0.7	435	2	Q8VYK9	Q8vyk9 arabidopsis
39	0.7	439	2	Q63160	Q63160 burkholderi
40	0.7	730	2	Q9VJ84	Q9vj84 drosophila
41	0.7	1081	2	Q9PNS7	Q9pns7 campylobact
42	0.7	1157	2	Q7Q2Y4	Q7q2y4 anopheles g
43	0.7	1286	1	PATC_DROME	P18502 drosophila
44	0.7	1318	2	Q9XYP5	Q9xyp5 junonia coe
45	0.7	1711	2	Q6F598	Q6f598 pyrococcus
46	0.7	64	2	Q6CRB4	Q6cbr4 kluyveromyc
47	0.7	64	2	Q9P8E2	Q9p8e2 kluyveromyc
48	0.7	67	2	Q9PIB8	Q9piB8 homo sapien
49	0.7	75	1	Y059_TREPA	Q83098 treponema p
50	0.7	81	1	IC47_CHV1E	Q8jp02 cercopitheci
51	0.7	89	2	Q8W5M5	Q8w5m5 oryza sativ
52	0.7	89	2	Q7XH79	Q7xh79 oryza sativ
53	0.7	94	2	Q8ULX2	Q8ulx2 pyrococcus
54	0.7	99	2	Q9JT54	Q9jts4 neisseria m
55	0.7	99	2	Q9JY69	Q9jy69 neisseria m
56	0.7	106	1	COLA_HORSE	P02704 equus cabal
57	0.7	108	1	COLB_HORSE	P02705 equus cabal
58	0.7	115	2	Q7V5Z5	Q7v5z5 prochloroco
59	0.7	123	2	Q8BNN7	Q8bnn7 mus musculu
60	0.7	126	2	Q8P7A2	Q8p7a2 xanthomonas
61	0.7	149	2	Q68E48	Q68e48 aeromonas p
62	0.7	162	2	Q9CWF0	Q9cwf0 mus musculu
63	0.7	183	2	Q75ET0	Q75et0 ashbya goss
64	0.7	186	2	Q8GB87	Q8geb7 mycobacteri
65	0.7	190	2	Q800L9	Q800l9 paralichthy
66	0.7	191	1	CRF_PIG	P06296 sus scrofa
67	0.7	191	2	Q8HZV1	Q8hzv1 sus scrofa
68	0.7	196	1	CRF_HUMAN	P06850 homo sapien
69	0.7	204	2	Q6BY40	Q6by40 debaryomyce
70	0.7	211	2	Q9YCB7	Q9ycb7 aeropyrum p
71	0.7	212	2	Q8E4Q2	Q8e4q2 streptococc
72	0.7	213	2	Q82HK2	Q82hk2 streptomyce
73	0.7	217	2	Q7X065	Q7x065 uncultured
74	0.7	226	2	Q74Z07	Q74z07 ashbya goss
75	0.7	227	2	Q6MPN0	Q6mpn0 bdellovibri
76	0.7	232	2	Q50183	Q50183 pseudomonas
77	0.7	240	2	Q6A557	Q6a557 propionibac
78	0.7	241	2	Q837I5	Q837i5 enterococcu
79	0.7	247	2	Q7X6M4	Q7x6m4 oryza sativ
80	0.7	251	2	Q7PXC3	Q7pxc3 anopheles g
81	0.7	259	2	Q73ZE4	Q73ze4 mycobacteri
82	0.7	262	2	Q9KDB1	Q9kdb1 bacillus ha
83	0.7	267	2	Q847J9	Q847j9 pseudomonas
84	0.7	276	2	Q8FR67	Q8fr67 corynebacte
85	0.7	278	2	Q72E37	Q72e37 desulfovibr
86	0.7	281	1	UPPP_CORST	Q9fb58 corynebacte
87	0.7	282	2	Q7QB93	Q7qb93 anopheles g
88	0.7	286	2	Q9SIL6	Q9sil6 arabidopsis
89	0.7	286	2	Q72CK4	Q72ck4 desulfovibr
90	0.7	296	2	Q8U210	Q8u210 pyrococcus
91	0.7	296	2	Q8Y3G5	Q8y3g5 ralstonia s
92	0.7	297	2	Q7N3M8	Q7n3m8 photorhabd
93	0.7	308	2	Q6UKF2	Q6ukf2 photonis ps
94	0.7	314	2	Q7SFG5	Q7sf55 neurospora
95	0.7	316	2	Q9BWQ6	Q9bwq6 homo sapien
96	0.7	320	2	Q58066	Q58066 pyrococcus
97	0.7	326	2	Q98DP1	Q98dp1 rhizobium l
98	0.7	331	2	Q8TVS6	Q8tvs6 methanopyru
99	0.7	337	2	Q9VQ95	Q9vq95 drosophila
100	0.7	337	2	Q72H23	Q72h23 thermus the

ALIGNMENTS

RESULT 1	
Q6UX14	PRELIMINARY; PRT; 1211 AA.
ID	Q6UX14
AC	Q6UX14; 2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Patched 2.
DE	Patched 2.
GN	ORFNames=UNQ560;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA	Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagte A.,
RA	Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA	Godowski P.;
RT	"The secreted protein discovery initiative (SPDI), a large-scale
RT	effort to identify novel human secreted and transmembrane proteins: a
RT	bioinformatics assessment.";
RL	Genome Res. 13:2265-2270(2003).
DR	ENBL; AY358555; AAQ88919.1; -.
DR	GO: 0016021; C: integral to membrane; IEA.
DR	GO: 0008158; F: hedgehog receptor activity; IEA.
DR	InterPro: IPR003392; Patched.
DR	InterPro: IPR004766; Patched_tm_recept.
DR	InterPro: IPR000731; SSD 5TM.
DR	Pfam: PF02460; Patched; I.
DR	TIGRFAMs: TIGR00918; 2A060602; 1.
DR	PROSITE: PS0156; SSD; 1.
DR	SEQUENCE 1211 AA; 13156 MW; 303D4FC5D39FB77 CRC64;
Query Match 100.0%; Score 1203; DB 2; Length 1211;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 1203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLFSLGCGIQRHCGKVL 60
Db	1 MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLFSLGCGIQRHCGKVL 60
Qy	61 LGLAFAGALGLRMAIETNLEQLWVEGSRVSVQELHYTKELGEEAAYTSQMLIQAR 120
Db	61 LGLAFAGALGLRMAIETNLEQLWVEGSRVSVQELHYTKELGEEAAYTSQMLIQAR 120
Qy	121 QEGENILTPPALGHLQAALTASKVQVSLYKSKWDLNKKIYKSGVPLIENGMIEMLEKL 180
Db	121 QEGENILTPPALGHLQAALTASKVQVSLYKSKWDLNKKIYKSGVPLIENGMIEMLEKL 180
Qy	181 FPCVILTPDLDFWEGAKLQGSAYLPGRPDIQTNLDPQLLEELGPFASLEGFRELDDK 240
Db	181 FPCVILTPDLDFWEGAKLQGSAYLPGRPDIQTNLDPQLLEELGPFASLEGFRELDDK 240
Qy	241 AQVQAVYGRPCPLHDDLHCPSPAPNHSROAPNVAHELGGCHGFGSHKFMHWOELLG 300
Db	241 AQVQAVYGRPCPLHDDLHCPSPAPNHSROAPNVAHELGGCHGFGSHKFMHWOELLG 300
Qy	301 GMARDPQELLRAEALSTFLMSPROLVYHFRGDYQTHDIGWSEEQASTVLQAWRRFV 360
Db	301 GMARDPQELLRAEALSTFLMSPROLVYHFRGDYQTHDIGWSEEQASTVLQAWRRFV 360
Qy	361 QLAQALPENASQIHAFSSTLDDILHAFSEVSAARVVGGLMLLAYACVYMLRWDCAQ 420
Db	361 QLAQALPENASQIHAFSSTLDDILHAFSEVSAARVVGGLMLLAYACVYMLRWDCAQ 420
RESULT 2	
PTC2 HUMAN	
ID	PTC2 HUMAN STANDARD; PRT; 1203 AA.
AC	Q9Y6C5; O95341; O95856;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Patched protein homolog 2 (PTC2).
GN	Name=PTCH2;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORM 1).
RP	MEDLINE=99030620; PubMed=9811851; DOI=10.1073/pnas.95.23.13630;


```
QY 121 QEGENILTPALGLHQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
Db |||
QY 121 QEGENILTPALGLHQAALTASKVQVSLYKGSWDLNKICYKSGVPLIENGMIEMIEKL 180
Db |||
QY 181 FPCVILTPDLPCFWEGAKLOGSSAYLPGRPDIQWNTLDPQLLEELGFPFASLEGFRELDDK 240
Db |||
QY 241 AQVGQAVYGRPCPLHPDDLHCPSAPNHSRQAPNVAHELSCGGCHGSHKFMHQEBELLG 300
Db |||
QY 241 AQVGQAVYGRPCPLHPDDLHCPSAPNHSRQAPNVAHELSCGGCHGSHKFMHQEBELLG 300
QY 301 GMARDPOGELLRAEALQSTLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWORRFV 360
Db |||
QY 301 GMARDPOGELLRAEALQSTLLMSPROLYEHFRGDYQTHDIGWSEEQASTVLQAWORRFV 360
QY 361 QLAQEAALPENASQOIHAFFSSTLDDILHAFSEVSAAARVVGYYLLMLAYACVTMLRWDCAQ 420
Db |||
QY 361 QLAQEAALPENASQOIHAFFSSTLDDILHAFSEVSAAARVVGYYLLMLAYACVTMLRWDCAQ 420
QY 421 SQGSVGLAGVLLVALAVASGLIGCALIGITFNATTOVLPLFALGIGVDVFLLAHAFTE 480
Db |||
QY 421 SQGSVGLAGVLLVALAVASGLIGCALIGITFNATTOVLPLFALGIGVDVFLLAHAFTE 480
QY 481 ALPCTPQOERWGECLQRTGTSVVLTSINNMAAFIIMAAALVPIPALRAPSLQAAIVVGCTFV 540
Db |||
QY 481 ALPCTPQOERWGECLQRTGTSVVLTSINNMAAFIIMAAALVPIPALRAPSLQAAIVVGCTFV 540
QY 541 AVMLVFPFALLSLDLRRRHRCQRLDVLCCFSSPCSQAQVIQILPQELGDCQTPVPGIAHATATV 600
Db |||
QY 541 AVMLVFPFALLSLDLRRRHRCQRLDVLCCFSSPCSQAQVIQILPQELGDCQTPVPGIAHATATV 600
QY 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDLGSELFPSPGGSTRDLGQEBETRQKAACKS 660
Db |||
QY 601 QAFTHCEASSQHVVTILPPOAHLVPPSPDLGSELFPSPGGSTRDLGQEBETRQKAACKS 660
QY 661 LPCARWNLHAFARYQFAPLLQLSHAKAIVLVLFCALIGLSLYGATLVQDGLATDVVVRPG 720
Db |||
QY 661 LPCARWNLHAFARYQFAPLLQLSHAKAIVLVLFCALIGLSLYGATLVQDGLATDVVVRPG 720
QY 721 TKEHAFLSAQURLYFSLYEVALVTQGGFDYAHRSQALFDLHQRFSLSKXAVLPPPATQAPRT 780
Db |||
QY 721 TKEHAFLSAQURLYFSLYEVALVTQGGFDYAHRSQALFDLHQRFSLSKXAVLPPPATQAPRT 780
QY 781 WLHYRNWLOGIOAAFQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDPSQLT 840
Db |||
QY 781 WLHYRNWLOGIOAAFQDQWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDPSQLT 840
QY 841 TRKLVDREGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPPPEWLHDKYDTTGENLRIP 900
Db |||
QY 841 TRKLVDREGLIPPELFYMGLTVMVSSDPLGLAASQANFYPPPPPEWLHDKYDTTGENLRIP 900
QY 901 PAQPLEPAQFPFLRLGLQKTADFVEATEGARAAACAEAGQAGVHAYPGSPGPFLEWQYIGL 960
Db |||
QY 901 PAQPLEPAQFPFLRLGLQKTADFVEATEGARAAACAEAGQAGVHAYPGSPGPFLEWQYIGL 960
QY 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGILVILVAMMTVELFPGMFLGFIKLSAIPV 1020
Db |||
QY 961 RRCFLAVCILLVCTFLVCALLLNPNWTAGILVILVAMMTVELFPGMFLGFIKLSAIPV 1020
QY 1021 ILVASVGIGVEFTVHVVALGFLTTQGSNLRRAHALEHTFAPVTDGALSTLLGLMLAGSH 1080
Db |||
QY 1021 ILVASVGIGVEFTVHVVALGFLTTQGSNLRRAHALEHTFAPVTDGALSTLLGLMLAGSH 1080
QY 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLISILSGPPPEVIQMYKESPEILSPAPOGGG 1140
Db |||
QY 1081 FDFIVRYFFAALTVLTLGLLHGLVLLPVLISILSGPPPEVIQMYKESPEILSPAPOGGG 1140
QY 1141 LRWGASSLSPOSFARVTTSMVTVAIHPDPLPGAYIHPADDEPPWSPAAATSSGNSSRGPGP 1200
Db |||
QY 1141 LRWGASSLSPOSFARVTTSMVTVAIHPDPLPGAYIHPADDEPPWSPAAATSSGNSSRGPGP 1200
QY 1201 ATG 1203
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Db 1201 ATG 1203

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|||
Db 1201 ATG 1203
|||
RESULT 3
PTC2 MOUSE
ID_PTC2 MOUSE STANDARD; PRT; 1182 AA.
AC O35535;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Patched protein homolog 2 (PTC2).
GN Name=Ptc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=98122566; PubMed=9462734;
RA Motoyama J., Takabatake T., Takeshima K., Hui C.-C.;
RT "Ptc2, a second mouse patched gene is co-expressed with Sonic
RT hedgehog."
RL Nat. Genet. 18:104-106(1998).
RN [2]
RP SEQUENCE OF 196-446 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Neuroretina;
RX MEDLINE=97379366; PubMed=9237688; DOI=10.1016/S0014-5793(97)00645-5;
RA Takabatake T., Ogawa M., Takahashi T.C., Mizuno M., Okamoto M.,
RA Takeshima K.;
RT Hedgehog and patched gene expression in adult ocular tissues."
RL FEBS Lett. 410:485-489(1997).
CC -1- FUNCTION: May have a role in epidermal development. May act as a
CC receptor for Sonic hedgehog (SHH).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in epithelial cells of the
CC developing hair, tooth and whisker.
CC -1- DEVELOPMENTAL STAGE: Detected in 8.5 to 17.5 dpc embryos.
CC -1- SIMILARITY: Belongs to the patched family.
CC -1- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC -----
CC EMBL; AB010833; BAA24691.1; -.
CC PIR; T13952; T13952.
CC MGD; MGI:1095405; Ptc2.
CC InterPro; IPR003392; Patched.
CC InterPro; IPR004766; Patchedtm_recept.
CC InterPro; IPR000731; SSD_5TM.
CC Pfam; PF02460; Patched; 1.
CC TIGRFAMS; TIGR00918; 2A060602; 1.
CC PROSITE; PS50156; SSD; 1.
CC Glycoprotein; Receptor; Transmembrane.
KW DOMAIN 1 57 Cytoplasmic (Potential).
FT TRANSMEM 58 78 Potential.
FT DOMAIN 79 394 Extracellular (Potential).
FT TRANSMEM 395 414 Potential.
FT DOMAIN 415 428 Cytoplasmic (Potential).
FT TRANSMEM 429 449 Potential.
FT DOMAIN 450 457 Extracellular (Potential).
FT TRANSMEM 458 478 Potential.
FT DOMAIN 479 501 Cytoplasmic (Potential).
FT TRANSMEM 502 522 Potential.
FT DOMAIN 523 531 Extracellular (Potential).
FT TRANSMEM 532 552 Potential.
FT DOMAIN 553 686 Cytoplasmic (Potential).
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FT TRANSMEM 687 707 Potential.
FT DOMAIN 708 963 Extracellular (Potential).
FT TRANSMEM 964 984 Potential.
FT DOMAIN 985 991 Cytoplasmic (Potential).
FT TRANSMEM 992 1012 Potential.
FT DOMAIN 1013 1034 Extracellular (Potential).
FT TRANSMEM 1034 1034 Potential.
FT DOMAIN 1035 1064 Cytoplasmic (Potential).
FT TRANSMEM 1065 1085 Potential.
FT DOMAIN 1086 1086 Extracellular (Potential).
FT TRANSMEM 1087 1107 Potential.
FT DOMAIN 1108 1182 Cytoplasmic (Potential).
FT TRANSMEM 1182 1182 SSD.
FT DOMAIN 394 552 SSD.
FT CARBOHYD 370 370 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 812 812 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1182 AA; 128585 MW; 715233D912C352F2 CRC64;

Query Match 7.8%; Score 94; DB 1; Length 1182;
Best Local Similarity 100.0%; Pred. No. 4.9e-82;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 693 FGALGSLGATLVQDGLATDVVPRGTKEHAFSLAQRYFSLYEVALVTGGEDYVHVS 752
Db 693 FGALGSLGATLVQDGLATDVVPRGTKEHAFSLAQRYFSLYEVALVTGGEDYVHVS 752

Qy 753 QRALFDLHQRFSSLKAVLPPPPATQAPRTWLHYR 786
Db 753 QRALFDLHQRFSSLKAVLPPPPATQAPRTWLHYR 786

RESULT 4
Q90XB9 PRELIMINARY; PRT; 913 AA.
AC Q90XB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Patched 2 (Fragment).
GN Name=PTC2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Parse R.V. Jr., Vogan K.J., Tabin C.J.;
RT "Ptc1 and Ptc2 Transcripts Provide Distinct Readouts of Hedgehog
RT Signaling Activity during Chick Embryogenesis.";
RL Dev. Biol. 0:0-0(2001).
DR EMBL; AF409095; AAK97655.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
DR Pfam; PF02460; Patched; 1.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
FT NON TER 913
FT SEQUENCE 913 AA; 101047 MW; DBD8117E5D842F33 CRC64;

Query Match 3.2%; Score 38; DB 2; Length 913;
Best Local Similarity 100.0%; Pred. No. 2.4e-27;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 MIEKLFPCVILTPDLCFEWAGKLGGSAYLFGRPDIQW 213
Db 172 MIEKLFPCVILTPDLCFEWAGKLGGSAYLFGRPDIQW 209

RESULT 5
PTC1_BRARE STANDARD; PRT; 1220 AA.
AC Q98864;
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Patched protein homolog 1 (Patched 1) (PTC1).
GN Name=ptcl;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
RN NCBI_TaxID=7955;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=96379744; PubMed=8787757;
RA Concordet J.-P., Lewis K.E., Moore J.W., Goodrich L.V., Johnson R.L.,
RA Scott M.P., Ingham P.W.;
RT "Spatial regulation of the zebrafish patched homologue reflects the
RT roles of sonic hedgehog and protein kinase A in neural tube and somite
RT patterning.";
RL Development 122:2835-2846(1996).
CC -|- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
CC hedgehog (IHH) and desert hedgehog (DHH). Associates with the
CC smoothened protein (SMO) to transduce the hedgehog's proteins
CC signal (By similarity).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- TISSUE SPECIFICITY: Detected in embryonic presomitic mesoderm,
CC neuroectoderm, tissue surrounding the notochord, ventral neural
CC tube.
CC -|- DEVELOPMENTAL STAGE: At all stages, expression corresponds to the
CC localization of SHH. First detected during gastrulation. By 36
CC hours, PTC1 appears in the first branchial arch and the posterior
CC mesenchyme of the fin bud; by 48 hours, in the hindbrain and
CC foregut.
CC -|- INDUCTION: Activated by Sonic hedgehog.
CC -|- PTM: Glycosylation is necessary for SHH binding (By similarity).
CC -|- SIMILARITY: Belongs to the patched family.
CC -|- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
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EMBL: X98883; CAA67386.1; -.
DR PIR; T18291; T18291.
DR ZFIN; ZDB-GENE-980526-44; ptcl.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD_5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRFAMs; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
DR KEGG; Glycocalyx; Receptor; Transmembrane.
FT DOMAIN 1 84 Cytoplasmic (Potential).
FT TRANSMEM 85 105 Potential.
FT DOMAIN 106 419 Extracellular (Potential).
FT TRANSMEM 420 440 Potential.
FT DOMAIN 441 449 Cytoplasmic (Potential).
FT TRANSMEM 450 470 Potential.
FT DOMAIN 471 484 Extracellular (Potential).
FT TRANSMEM 485 505 Potential.
FT DOMAIN 506 528 Cytoplasmic (Potential).
FT TRANSMEM 529 549 Potential.
FT DOMAIN 550 558 Extracellular (Potential).
FT TRANSMEM 559 579 Potential.
FT DOMAIN 580 739 Cytoplasmic (Potential).
FT TRANSMEM 740 760 Potential.
FT DOMAIN 761 1016 Extracellular (Potential).
FT TRANSMEM 1017 1037 Potential.
FT DOMAIN 1038 1044 Cytoplasmic (Potential).
FT TRANSMEM 1045 1065 Potential.

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FT DOMAIN 1066 1072 Extracellular (Potential).
 FT TRANSEM 1073 1093 Potential.
 FT DOMAIN 1094 1110 Cytoplasmic (Potential).
 FT TRANSEM 1111 1131 Potential.
 FT DOMAIN 1132 1143 Extracellular (Potential).
 FT TRANSEM 1144 1164 Potential.
 FT DOMAIN 1165 1220 Cytoplasmic (Potential).
 FT DOMAIN 421 579 SSD.
 FT DOMAIN 624 695 Thr-rich.
 FT CARBOHYD 397 397 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 865 865 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 888 888 N-linked (GLCNAC. . .) (Potential).
 SQ SEQUENCE 1220 AA; 135544 MW; D10A9D041159532D CRC64;

Query Match 1.7%; Score 20; DB 1; Length 1220;

Best Local Similarity 100.0%; Pred. No. 1.2e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 GGYLLMLAYACVTLRWDC 419

Db 427 GGYLLMLAYACVTLRWDC 446

RESULT 6

Q9DEF3 ID Q9DEF3 PRELIMINARY; PRT; 1413 AA.

AC Q9DEF3

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Patched-2.

GN Name=xptch-2;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20500895; PubMed=11044611; DOI=10.1016/S0925-4773(00)00436-6;

RA Takabatake T., Takahashi T.C., Takabatake Y., Yamada K., Ogawa M.,

RA Takashima K.;

RT "Distinct expression of two types of Xenopus Patched genes during

early embryogenesis and hindlimb development.";

RL Mech. Dev. 98:99-104(2000).

DR EMBL; AB037688; BAB18575.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0008158; F:hedgehog receptor activity; IEA.

DR InterPro; IPR003392; Patched

DR InterPro; IPR004766; Patchedtm_recept.

DR InterPro; IPR000731; SSD_5TM.

DR Pfam; PF02460; Patched; 1.

DR TIGRFAMs; TIGR00918; 2A060602; 1.

DR PROSITE; PS50156; SSD; 1.

SQ SEQUENCE 1413 AA; 157372 MW; 1215D2D7733B7F17 CRC64;

Query Match 1.7%; Score 20; DB 2; Length 1413;

Best Local Similarity 100.0%; Pred. No. 1.4e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALGIGVDD 470

Db 476 FNAATTQVLPLALGIGVDD 495

RESULT 7

Q6IRA5 ID Q6IRA5 PRELIMINARY; PRT; 1422 AA.

AC Q6IRA5

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX TISSUE=Embryo;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RX TISSUE=Embryo;

RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative.";

RL Dev. Dyn. 225:384-391(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Embryo;

RC Klein S., Strausberg R.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC070995; AAH70995.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0008158; F:hedgehog receptor activity; IEA.

DR InterPro; IPR003392; Patched

DR InterPro; IPR004766; Patchedtm_recept.

DR InterPro; IPR000731; SSD_5TM.

DR Pfam; PF02460; Patched; 1.

DR TIGRFAMs; TIGR00918; 2A060602; 1.

DR PROSITE; PS50156; SSD; 1.

KW Hypothetical protein.

SQ SEQUENCE 1422 AA; 158128 MW; 2884B2656E60CE72 CRC64;

Query Match 1.7%; Score 20; DB 2; Length 1422;

Best Local Similarity 100.0%; Pred. No. 1.4e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLPLALGIGVDD 470

Db 476 FNAATTQVLPLALGIGVDD 495

RESULT 8

PTC2 CYNPY ID_PTC2 CYNPY STANDARD; PRT; 255 AA.

AC Q42334;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Patched protein homolog 2 (PTC2) (Fragment).

GN Name=PTC2;

OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neuroretina;
 RX MEDLINE=97379366; PubMed=9237688; DOI=10.1016/S0014-5793(97)00645-5;
 RA Takabatake T., Ogawa M., Takahashi T.C., Mizuno M., Okamoto M.,
 RA Takashima K.;
 RT "Hedgehog and patched gene expression in adult ocular tissues.";
 RL FEBS Lett. 410:485-489(1997).
 CC -!- FUNCTION: May act as a receptor for sonic hedgehog (SHH).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: In the eye, detected in neural retina, iris,
 CC retinal pigment epithelium, but not in lens.
 CC -!- INDUCTION: Activated by hedgehog.
 CC -!- SIMILARITY: Belongs to the patched family.
 CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
 CC -----
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 CC -----
 CC EMBL: AB000846; BAA23305.1; -.
 CC InterPro: IPR000731; SSD_5TM.
 CC PROSITE: PS50156; SSD; 1.
 CC Glycoprotein; Receptor; Transmembrane.
 FT NON_TER 1 1
 FT DOMAIN <1 197 Extracellular (Potential).
 FT TRANSMEM 198 218 Potential.
 FT DOMAIN 219 227 Cytoplasmic (Potential).
 FT TRANSMEM 228 248 Potential.
 FT DOMAIN 249 >255 Extracellular (Potential).
 FT DOMAIN 199 >255 SSD.
 FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 175 175 N-linked (GlcNAc...) (Potential).
 FT NON_TER 255 255
 FT SEQUENCE 255 AA; 28391 MW; 715139F607403CB2 CRC64;
 Query Match 1.6%; Score 19; DB 1; Length 255;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 400 GGYLLMLAYACVTLRWDC 418
 Db |||||
 205 GGYLLMLAYACVTLRWDC 223
 RESULT 9
 Q8MKB3 PRELIMINARY; PRT; 234 AA.
 ID Q8MKB3
 AC Q8MKB3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Patched (Fragment).
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Semevolos S.A., Nixon A.J.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF510667; AAM34780.1; -.
 DR InterPro: IPR000731; SSD_5TM.
 DR PROSITE; PS50156; SSD; 1.
 FT NON_TER 1 1

FT NON_TER 234 234
 SQ SEQUENCE 234 AA; 25455 MW; 614715710DD43B2C CRC64;
 Query Match 1.2%; Score 15; DB 2; Length 234;
 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 451 FNAATTQVLPLFALG 465
 Db |||||
 218 FNAATTQVLPLFALG 232
 RESULT 10
 Q9Z2A1 PRELIMINARY; PRT; 608 AA.
 ID Q9Z2A1
 AC Q9Z2A1;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Patched (Fragment).
 GN Name=ptc;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Hypothalamus;
 RC Zhao P., Roy N.K., Xu G., Burns F.J.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF079162; AAC99398.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
 DR InterPro: IPR003392; Patched.
 DR InterPro: IPR000731; SSD_5TM.
 DR PFAM; PF02460; Patched; 1.
 DR PROSITE; PS50156; SSD; 1.
 FT NON_TER 608 608
 FT SEQUENCE 608 AA; 67327 MW; 73F505A1512EE9C5 CRC64;
 Query Match 1.2%; Score 15; DB 2; Length 608;
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 451 FNAATTQVLPLFALG 465
 Db |||||
 481 FNAATTQVLPLFALG 495
 RESULT 11
 Q6TKP9 PRELIMINARY; PRT; 651 AA.
 ID Q6TKP9
 AC Q6TKP9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Patched (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mansilla M.A., Vieira A.R., Murray J.C.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY395759; AAR21239.1; JOINED.
 DR EMBL; AY395760; AAR21239.1; JOINED.
 DR EMBL; AY395761; AAR21239.1; JOINED.
 DR EMBL; AY395763; AAR21239.1; JOINED.
 DR EMBL; AY395765; AAR21239.1; JOINED.
 DR EMBL; AY395767; AAR21239.1; JOINED.
 DR EMBL; AY395768; AAR21239.1; JOINED.
 DR EMBL; AY395766; AAR21239.1; JOINED.

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DR EMBL; AY395764; AAR21239.1; JOINED.
DR EMBL; AY395762; AAR21239.1; JOINED.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR000731; SSD 5TM.
DR Pfam; PF02460; Patched; 2.
DR PROSITE; PS50156; SSD; 1.
FT NON_TER 1
FT NON_TER 651
SQ SEQUENCE 651 AA; 73252 MW; FBB9F08BBDA25868 CRC64;

Query Match 1.2%; Score 15; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLFPFLALG 465
DB 90 FNAATTQVLFPFLALG 104

RESULT 12
Q9DEF4 PRELIMINARY; PRT; 1239 AA.
ID Q9DEF4 AC Q9DEF4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Patched-1 (Fragment).
GN Name=Xptch-1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20500895; PubMed=11044611; DOI=10.1016/S0925-4773(00)00436-6;
RA Takabatake T., Takahashi T.C., Takabatake Y., Yamada K., Ogawa M.,
RT "Distinct expression of two types of Xenopus Patched genes during
RT early embryogenesis and hindlimb development.";
RL Mech. Dev. 98:99-104(2000).
DR EMBL; AB037686; BAB18574.2; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD 5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRfams; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
FT NON_TER 1239 1239
SQ SEQUENCE 1239 AA; 138127 MW; 069D4B4B8517E495 CRC64;

Query Match 1.2%; Score 15; DB 2; Length 1239;
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLFPFLALG 465
DB 485 FNAATTQVLFPFLALG 499

RESULT 13
Q9W6T6 PRELIMINARY; PRT; 1243 AA.
ID Q9W6T6 AC Q9W6T6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Patched-2 protein.
GN Name=ptc2; Synonyms=ptc1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lewis K.E., Concordet J.P., Ingham P.W.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ007742; CAB39726.1; -.
DR ZFIN; ZDB-GENE-980526-196; ptc2.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD 5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRfams; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
SQ SEQUENCE 1243 AA; 138548 MW; FABF459DB0C91371 CRC64;

Query Match 1.2%; Score 15; DB 2; Length 1243;
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLFPFLALG 465
DB 484 FNAATTQVLFPFLALG 498

RESULT 14
Q98SW6 PRELIMINARY; PRT; 1418 AA.
ID Q98SW6 AC Q98SW6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Patched-1.
GN Name=Ptc1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21095181; PubMed=11165486; DOI=10.1016/S0925-4773(00)00526-8;
RA Koebernick K., Hollemann T., Pieler T.;
RT "Molecular cloning and expression analysis of the Hedgehog receptors
RT Xptc1 and Xsmo in Xenopus laevis.";
RL Mech. Dev. 100:303-308(2001).
DR EMBL; AF302765; AAK15463.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR004766; Patchedtm_recept.
DR InterPro; IPR000731; SSD 5TM.
DR Pfam; PF02460; Patched; 1.
DR TIGRfams; TIGR00918; 2A060602; 1.
DR PROSITE; PS50156; SSD; 1.
SQ SEQUENCE 1418 AA; 158226 MW; 4FEA30C2D5031F54 CRC64;

Query Match 1.2%; Score 15; DB 2; Length 1418;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 451 FNAATTQVLFPFLALG 465
DB 485 FNAATTQVLFPFLALG 499

RESULT 15
PTC1_MOUSE
ID PTC1_MOUSE STANDARD; PRT; 1434 AA.
AC Q6115;

```


[4] VARIANTS BCNS TYR-513 AND ARG-1069.
 RX MEDLINE=97136566; PubMed=9981943;
 RA Wicking C., Shanley S., Smyth I., Gillies S., Negus K., Graham S.,
 RA Suhera G., Hautes N., Edwards M., Mainwright B.J.,
 RA Chenevix-Trench G.;
 RT "Most germ-line mutations in the nevoid basal cell carcinoma syndrome
 RT lead to a premature termination of the PATCHED protein, and no
 RT genotype-phenotype correlations are evident.";
 RL Am. J. Hum. Genet. 60:21-26(1997).
 [5]
 RP VARIANT NBCCS ASP-1438.
 RX MEDLINE=98001068; PubMed=9341860;
 RA Lench N.J., Telford E.A.R., High A.S., Markham A.P., Wicking C.,
 RA Mainwright B.J.;
 RT "Characterisation of human patched germ line mutations in naevoid
 RT basal cell carcinoma syndrome.";
 RL Hum. Genet. 100:497-502(1997).
 [6]
 RP VARIANT PRO-1315.
 RX MEDLINE=99211211; PubMed=10200051;
 RX DOI=10.1002/(SICI)1098-1004(1998)11:6<480::AID-HUMU9-3.3.CO;2-W;
 RA Hasenpusch-Theil K., Bataille V., Laehdette J., Obermayr F.,
 RA Sampson J.R., Frischauf A.-M.;
 RT "Gorlin syndrome: Identification of 4 novel germ-line mutations of the
 RT human patched (PTCH) gene.";
 RL Hum. Mutat. 11:480-480(1998).
 [7]
 RP VARIANTS BCNS SER-376 AND VAL-1083 INS, AND VARIANT BCC TRP-1114.
 RX MEDLINE=98281604; PubMed=9620294;
 RA Aszterbaum M., Rothman A.L., Johnson R.L., Fisher M., Xie J.,
 RA Bonifas J.M., Zhang X., Scott M.P., Epstein E.H. Jr.;
 RT "Identification of mutations in the human PATCHED gene in sporadic
 RT basal cell carcinomas and in patients with the basal cell nevus
 RT syndrome."; Dermatol. 110:885-888(1998).
 [8]
 RL J. Invest. Dermatol. 110:885-888(1998).
 [9]
 RP VARIANT PRO-1315.
 RX MEDLINE=20334946; PubMed=10874314;
 RX DOI=10.1002/1098-1004(200007)16:1<89::AID-HUMU18-3.3.CO;2-Z;
 RA Dong J., Gallani M.R., Pomeroy S.L., Reardon D., Bale A.E.;
 RT "Identification of PATCHED mutations in medulloblastomas by direct
 RT sequencing.";
 RL Hum. Mutat. 16:89-90(2000).
 [10]
 RP VARIANT BCNS PRO-1132.
 RX MEDLINE=21151106; PubMed=11231326;
 RA Reifemberger J., Arnold N., Kiechle M., Reifemberger G., Hauschild A.;
 RT "Coincident PTCH and BRCA1 germline mutations in a patient with nevoid
 RT basal cell carcinoma syndrome and familial breast cancer.";
 RL J. Invest. Dermatol. 116:472-474(2001).
 [11]
 RP VARIANTS SQUAMOUS CELL CARCINOMA MET-829 AND LYS-1242.
 RX MEDLINE=21184537; PubMed=11286632;
 RA Ping X.L., Ratner D., Zhang H., Wu X.L., Zhang M.J., Chen F.F.,
 RA Silvers D.N., Peacocke M., Tsou H.C.;
 RT "PTCH mutations in squamous cell carcinoma of the skin.";
 RL J. Invest. Dermatol. 116:614-616(2001).
 [12]
 CC -!- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
 CC hedgehog (IHH) and desert hedgehog (DHH). Associates with the
 CC smoothened protein (SMO) to transduce the hedgehog's proteins
 CC signal. Seems to have a tumor suppressor function, as inactivation
 CC of this protein is probably a necessary, if not sufficient step
 CC for tumorigenesis.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: In the adult, expressed in brain, lung, liver,
 CC heart, placenta, skeletal muscle, pancreas and kidney. Expressed
 CC in tumor cells but not in normal skin.
 CC -!- DEVELOPMENTAL STAGE: In the embryo, found in all major target
 CC tissues of sonic hedgehog, such as the ventral neural tube,
 CC somites, and tissues surrounding the zone of polarizing activity
 CC of the limb bud.
 CC -!- PTM: Glycosylation is necessary for SHH binding (By similarity).

CC -!- DISEASE: Defects in PTCH are probably the cause of basal cell
 CC nevus syndrome (BCNS) [MIM:109400]; also known as Gorlin syndrome
 CC or Gorlin-Goltz syndrome. BCNS is an autosomal dominant disease
 CC characterized by nevoid basal cell carcinomas (NBCCS) and
 CC developmental abnormalities such as rib and craniofacial
 CC alterations, polydactyly, syndactyly, and spina bifida. In
 CC addition, the patients suffer from a multitude of tumors like
 CC basal cell carcinomas (BCC), fibromas of the ovaries and heart,
 CC cysts of the skin, jaws and mesentery, as well as medulloblastomas
 CC and meningiomas. PTCH is also mutated in squamous cell carcinoma
 CC (SCC). Could also be associated with large body size observed in
 CC BCNS patients.
 CC -!- DISEASE: Defects in PTCH are a cause of sporadic basal cell
 CC carcinoma (BCC) [MIM:605462].
 CC -!- SIMILARITY: Belongs to the patched family.
 CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
 CC -!- DATABASE: NAME=PTCH mutation database;
 CC WWW="http://www.cybergene.se/PTCH/ptchbase.html".
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PTCH100.html".
 CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
 CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PTCH100.html".
 CC -!- SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U59464; AAC50550.1; --
 CC EMBL: U43148; AAC50496.1; --
 CC Genew: HGNC:9585; PTCH.
 CC MIM: 601309; --
 CC MIM: 109400; --
 CC MIM: 605462; --
 CC GO: GO:0005887; C: integral to plasma membrane; TAS.
 CC GO: GO:0004872; P: receptor activity; TAS.
 CC GO: GO:0008283; P: cell proliferation; TAS.
 CC GO: GO:0009653; P: morphogenesis; TAS.
 CC GO: GO:0007165; P: signal transduction; TAS.
 CC InterPro: IPR003392; Patched.
 CC InterPro: IPR004766; Patchedtm_recept.
 CC InterPro: IPR000731; SSD_5TM.
 CC Pfam: PF02460; Patched; 1.
 CC TIGRFAMs: TIGR00918; 2A060602; 1.
 CC PROSITE: PS50156; SSD; 1.
 CC Anti-oncogene; Disease mutation; Glycoprotein; Polymorphism; Receptor;
 CC Transmembrane.
 CC DOMAIN 1 100 Cytoplasmic (Potential).
 CC TRANSMEM 101 121 Potential.
 CC DOMAIN 122 436 Extracellular (Potential).
 CC TRANSMEM 437 457 Potential.
 CC DOMAIN 458 472 Cytoplasmic (Potential).
 CC TRANSMEM 473 493 Potential.
 CC DOMAIN 494 501 Extracellular (Potential).
 CC TRANSMEM 502 522 Potential.
 CC DOMAIN 523 547 Cytoplasmic (Potential).
 CC TRANSMEM 548 568 Potential.
 CC DOMAIN 569 577 Extracellular (Potential).
 CC TRANSMEM 578 598 Potential.
 CC DOMAIN 599 748 Cytoplasmic (Potential).
 CC TRANSMEM 749 769 Potential.
 CC DOMAIN 770 1027 Extracellular (Potential).
 CC TRANSMEM 1028 1048 Potential.
 CC DOMAIN 1049 1055 Cytoplasmic (Potential).
 CC TRANSMEM 1056 1076 Potential.
 CC DOMAIN 1077 1083 Extracellular (Potential).
 CC TRANSMEM 1084 1104 Potential.
 CC DOMAIN 1105 1121 Cytoplasmic (Potential).
 CC TRANSMEM 1122 1141 Potential.
 CC DOMAIN 1142 1154 Extracellular (Potential).
 CC TRANSMEM 1155 1175 Potential.
 CC DOMAIN 1176 1447 Cytoplasmic (Potential).

```

FT DOMAIN 14 31 Gly-rich.
FT DOMAIN 438 598 SSD.
FT CARBOHYD 141 141 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 312 312 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 349 349 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 414 414 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 875 875 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 1000 1000 N-linked (GlcNAc... ) (Potential).
FT VARIANT 175 175 L -> P (in BCNS; sporadic BCC).
FT VARIANT 376 376 /FTID=VAR_007843.
FT VARIANT 509 509 F -> S (in BCNS).
FT VARIANT 509 509 G -> R (in BCNS; could be a rare
Query Match 1.2%; Score 15; DB 1; Length 1447;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 451 FNAATTQVLPFLALG 465
Db 495 FNAATTQVLPFLALG 509
|||||

RESULT 19
Q86XG7 PRELIMINARY; PRT; 183 AA.
AC Q86XG7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043542; AAH43542.1; -.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20842 MW; ACACB6FBFB7947D07 CRC64;

Query Match 1.1%; Score 13; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 187 TPLDCFWEAGKLQ 199
Db 164 TPLDCFWEAGKLQ 176
|||||

RESULT 20
Q9DDZ0 PRELIMINARY; PRT; 287 AA.
AC Q9DDZ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Patched-1 (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461147; PubMed=11003839;
RA Brewster R., Mullor J.L., Ruiz I Altaba A.;
RT "Gliz functions in FGF signaling during antero-posterior patterning.";
RL Development 127:4395-4405(2000).
DR EMBL; AF254386; AAG45954.1; -.
DR InterPro; IPR000731; SSD_5TM.
DR PROSITE; PS50156; SSD; 1.
FT NON_TER 1 1
FT NON_TER 287 287
SQ SEQUENCE 287 AA; 31800 MW; E2E8590EAD2F6474 CRC64;

Query Match 1.0%; Score 12; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 0.025; 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

Qy 188 PLDCFWEAGKLQ 199
Db 9 PLDCFWEAGKLQ 20
|||||

RESULT 21
Q66PH3 PRELIMINARY; PRT; 176 AA.
AC Q66PH3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Patched protein (Fragment).
GN Name=ptc2;
OS Astyanax fasciatus (Blind cave fish) (Astyanax mexicanus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Characiformes;
OC Characidae; Astyanax.
OX NCBI_TaxID=7994;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamamoto Y., Stock D.W., Jeffery W.R.;
RT "Hedgehog Signaling Controls Eye Degeneration in Blind Cavefish.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY661434; AAU04949.1; -.
FT NON_TER 1 1
FT NON_TER 176 176
SQ SEQUENCE 176 AA; 19885 MW; 9514D1B9C5BE3ACA CRC64;

Query Match 0.9%; Score 11; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 197 KLOGGSAYLPG 207
Db 43 KLOGGSAYLPG 53
|||||

RESULT 22

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PTC1_CYNPY
ID PTC1_CYNPY STANDARD; PRT; 257 AA.
AC Q42335;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Patched protein homolog 1 (PTC1) (Fragment).
GN Name=PTC1;
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroretina;
RX MEDLINE=97379366; PubMed=9237688; DOI=10.1016/S0014-5793(97)00645-5;
RA Takabatake T., Ogawa M., Takahashi T.C., Mizuno M., Okamoto M.,
RA Takeshima K.;
RL "Hedgehog and patched gene expression in adult ocular tissues.";
RL FEBS Lett. 410:485-489(1997).
CC -!- FUNCTION: Acts as a receptor for sonic hedgehog (SHH), indian
CC hedgehog (IHH) and desert hedgehog (DHH). Associates with the
CC smoothened protein (SMO) to transduce the hedgehog's proteins
CC signal (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: In the eye, detected in neural retina, iris,
CC retinal pigment epithelium, but not in lens.
CC -!- INDUCTION: Activated by Sonic hedgehog.
CC -!- PTM: Glycosylation is necessary for SHH binding (By similarity).
CC -!- SIMILARITY: Belongs to the patched family.
CC -!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB000848; BAA21678.1; -.
DR InterPro; IPR000731; SSD_5TM.
DR PROSITE; PS0156; SSD; 1.
KW Glycoprotein; Receptor; Transmembrane.
FT NON_TER 1 1 Extracellular (Potential).
FT DOMAIN <1 199 Potential.
FT TRANSMEM 200 220 Potential.
FT DOMAIN 221 235 Cytoplasmic (Potential).
FT TRANSMEM 236 256 Potential.
FT DOMAIN 201 >257 SSD.
FT CARBOHYD 75 75 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 177 177 N-linked (GlcNAc...) (Potential).
FT NON_TER 257 257
SQ SEQUENCE 257 AA; 28480 MW; 81C00FCC85D4633C CRC64;

Query Match 0.9%; Score 11; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

Qy 425 VGLAGVLVAL 435
Db 232 VGLAGVLVAL 242

RESULT 23
Q09540
ID Q09540 PRELIMINARY; PRT; 667 AA.
AC Q09540;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Patched family protein 2.
```

```
GN Name=ptc-2; ORFNames=F21H12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Favello A., R Wilson.;
RT "The sequence of C. elegans cosmid F21H12.";
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U23176; AAC46717.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008158; F:hedgehog receptor activity; IEA.
SQ SEQUENCE 667 AA; 73550 MW; BBBFB21B8A37EC15 CRC64;

Query Match 0.9%; Score 11; DB 2; Length 667;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1026 VGIGVEFTVHV 1036
Db 613 VGIGVEFTVHV 623

RESULT 24
PTC1_CAEEL
ID PTC1_CAEEL STANDARD; PRT; 1405 AA.
AC Q09614;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Patched protein homolog 1.
GN Name=ptc-1; ORFNames=2K675.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX MEDLINE=20381004; PubMed=10921907;
RA Kuwabara P.E., Lee M.-H., Schedl T., Jefferis G.S.X.E.;
RT "A C. elegans patched gene, ptc-1, functions in germ-line
RT cytokinesis";
RL Genes Dev. 14:1933-1944(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- FUNCTION: Required but not essential for cytokinesis of
```

mitotically proliferating germ cells.
-!- SUBCELLULAR LOCATION: Integral membrane protein; highly concentrated in a punctate pattern at the apices and internal membranes adjacent to the rachis. Expression is more intense in the distal proliferative region and in oocytes of the gonad arm.
-!- TISSUE SPECIFICITY: Germ line and its progenitors.
-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
-!- MISCELLANEOUS: Membrane proteins Patch and Smoothened form a receptor complex that binds Hedgehog morphogens. Despite the lack of Hh and Shc homologs, ptc-1 is still found to be functional. Absence of ptc-1 leads to the formation of multinucleate germ cells and sterility.
-!- SIMILARITY: Belongs to the patched family.
-!- SIMILARITY: Contains 1 sterol-sensing (SSD) domain.

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EMBL; Z46812; CAA86843.1; -
PIR; T27969; T27969
GermOnline; 209440; -
WormBase; WBGene0004208; ptc-1.
WormPep; ZK675.1; CE01720.
InterPro; IPR003392; Patched.
InterPro; IPR000731; SSD 5TM.
Pfam; PF02460; Patched; 1.
PROSITE; PS50156; SSD; 1.
Cell cycle; Cell division; Mitosis; Transmembrane.
FT DOMAIN 1 646
FT DOMAIN 647 667
FT DOMAIN 668 683
FT DOMAIN 684 704
FT DOMAIN 705 706
FT TRANSMEM 707 727
FT TRANSMEM 728 762
FT TRANSMEM 763 783
FT TRANSMEM 784 792
FT TRANSMEM 793 813
FT TRANSMEM 814 898
FT TRANSMEM 899 919
FT TRANSMEM 920 1172
FT TRANSMEM 1173 1193
FT TRANSMEM 1194 1235
FT TRANSMEM 1236 1256
FT TRANSMEM 1257 1273
FT TRANSMEM 1274 1294
FT TRANSMEM 1295 1302
FT TRANSMEM 1303 1323
FT TRANSMEM 1324 1405
FT TRANSMEM 651 813
FT TRANSMEM 1405 1405
FT TRANSMEM 9529FBD7B552BF3E CRC64;
SEQUENCE 1405 AA; 155454 MW; 9529FBD7B552BF3E CRC64;

Query Match 0.9%; Score 11; DB 1; Length 1405;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1026 VGIGVEFTVHV 1036
Db 1242 VGIGVEFTVHV 1252
|||||

RESULT 25

Q6TKP8 PRELIMINARY; PRT; 345 AA.
AC Q6TKP8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Patched (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mansilla M.A., Vieira A.R., Murray J.C.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY395769; AAR21240.1; JOINED.
DR EMBL; AY395770; AAR21240.1; JOINED.
DR EMBL; AY395771; AAR21240.1; JOINED.
DR EMBL; AY395772; AAR21240.1; -
FT NON_TER 1 1
SQ SEQUENCE 345 AA; 37221 MW; 4475791C5A80A469 CRC64;
Query Match 0.8%; Score 10; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1081 FDFIVRYFFA 1090
Db 43 FDFIVRYFFA 52
|||||

RESULT 26

Q69ZL6 PRELIMINARY; PRT; 1243 AA.
AC Q69ZL6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIAAI337 protein (Fragment).
GN Names=MKIAAI337;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
Nagase T., Ohara O., Koga H.;
RT Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK173152; BAD32430.1; -
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0008158; F.hedgehog receptor activity; IEA.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR000731; SSD 5TM.
DR Pfam; PF02460; Patched; 1.
DR PROSITE; PS50156; SSD; 1.
FT NON_TER 1 1
SQ SEQUENCE 1243 AA; 136915 MW; 543ED23C350D5949 CRC64;

Query Match 0.8%; Score 10; DB 2; Length 1243;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1106 LLPVLLSILG 1115
Db 1059 LLPVLLSILG 1068
|||||

RESULT 27

Q6T3U3 PRELIMINARY; PRT; 1331 AA.
AC Q6T3U3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Niemann-Pick C1-like 1.
 GN Name=Npc1l1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Altmann S.W., Davis H.R. Jr., Zhu L.-J., Yao X., Hoos L.M.,
 RA Tezloff G., Iyer S.P.N., Maguire M., Golovko A., Zeng M., Wang L.,
 RA Murgolo N.J., Graziano M.P.;
 RT "Niemann-Pick C1-like 1 (NPC1l1) is critical for intestinal
 RL cholesterol absorption.";
 RL Science 0:0-0(2004).
 DR EMBL; AY437867; AAR97888.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008158; F:hedghog receptor activity; IEA.
 DR GO; GO:0030301; P:cholesterol transport; IEA.
 DR InterPro; IPR004765; NP C type.
 DR InterPro; IPR003392; Patched.
 DR InterPro; IPR000731; SSD_5TM.
 DR Pfam; PF02460; Patched; 1.
 DR TIGRFAMs; TIGR00917; 2A060601; 1.
 DR PROSITE; PS0156; SSD; 1.
 SQ SEQUENCE 1331 AA; 146414 MW; 2E10EF2E3A337F70 CRC64;

Query Match 0.8%; Score 10; DB 2; Length 1331;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
 Db 1248 TLLGLLHGLV 1257
 |||||

RESULT 28

Q6R3Q4
 ID Q6R3Q4 PRELIMINARY; PRT; 1332 AA.
 AC Q6R3Q4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE NPC1L1 splice variant (Niemann-Pick C1-like 1).
 GN Name=NPC1L1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20247253; PubMed=10783261; DOI=10.1006/geno.2000.6151;
 RA Davies J.P., Levy B., Ioannou Y.A.;
 RT "Evidence for a Niemann-pick C (NPC) gene family: identification and
 RL characterization of NPC1L1.";
 RL Genomics 65:137-145(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Davies J.P., Ioannou Y.A.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Altmann S.W., Davis H.R. Jr., Zhu L.-J., Yao X., Hoos L.M.,
 RA Tezloff G., Iyer S.P.N., Maguire M., Golovko A., Zeng M., Wang L.,
 RA Murgolo N.J., Graziano M.P.;
 RT "Niemann-Pick C1-like 1 (NPC1L1) is critical for intestinal
 RL cholesterol absorption.";
 RL Science 0:0-0(2004).
 DR EMBL; AY515256; AAS56939.1; -;
 DR EMBL; AY437865; AAR97886.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008158; F:hedghog receptor activity; IEA.

DR GO; GO:0030301; P:cholesterol transport; IEA.
 DR InterPro; IPR004765; NP C type.
 DR InterPro; IPR003392; Patched.
 DR InterPro; IPR000731; SSD_5TM.
 DR Pfam; PF02460; Patched; 1.
 DR TIGRFAMs; TIGR00917; 2A060601; 1.
 DR PROSITE; PS0156; SSD; 1.
 SQ SEQUENCE 1332 AA; 145762 MW; EPE94P80309C3BF2 CRC64;

Query Match 0.8%; Score 10; DB 2; Length 1332;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
 Db 1247 TLLGLLHGLV 1256
 |||||

RESULT 29

Q6T3U4
 ID Q6T3U4 PRELIMINARY; PRT; 1333 AA.
 AC Q6T3U4;
 DT 03-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Niemann-Pick C1-like 1.
 GN Name=Npc1l1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Altmann S.W., Davis H.R. Jr., Zhu L.-J., Yao X., Hoos L.M.,
 RA Tezloff G., Iyer S.P.N., Maguire M., Golovko A., Zeng M., Wang L.,
 RA Murgolo N.J., Graziano M.P.;
 RT "Niemann-Pick C1-like 1 (NPC1L1) is critical for intestinal
 RL cholesterol absorption.";
 RL Science 0:0-0(2004).
 DR EMBL; AY437866; AAR97887.1; -;
 DR GO; GO:0042632; P:cholesterol homeostasis; IMP.
 DR InterPro; IPR004765; NP C type.
 DR InterPro; IPR003392; Patched.
 DR InterPro; IPR000731; SSD_5TM.
 DR Pfam; PF02460; Patched; 1.
 DR TIGRFAMs; TIGR00917; 2A060601; 1.
 DR PROSITE; PS0156; SSD; 1.
 SQ SEQUENCE 1333 AA; 147130 MW; 7771520D9B352735 CRC64;

Query Match 0.8%; Score 10; DB 2; Length 1333;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
 Db 1248 TLLGLLHGLV 1257
 |||||

RESULT 30

Q9UHC9
 ID Q9UHC9 PRELIMINARY; PRT; 1359 AA.
 AC Q9UHC9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Niemann-Pick C1-like protein 1.
 GN Name=NPC1L1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20247253; PubMed=10783261; DOI=10.1006/geno.2000.6151;
RA Davies J.P., Levy B., Ioannou Y.A.;
RT "Evidence for a Niemann-pick C (NPC) gene family: identification and
RL characterization of NPC1L1";
RL Genomics 65:137-145(2000).
DR EMBL; AF192522; AAF20396.1; -.
DR Genew; HGNC:7896; NPC1L1.
DR GO; GO:0015918; P:sterol transport; TAS.
DR InterPro; IPR004765; NP_C type.
DR InterPro; IPR003392; Patched.
DR InterPro; IPR000731; SSD 5TM.
DR Pfam; PF02460; Patched; I.
DR TIGRFAMs; TIGR00917; 2A060601; 1.
DR PROSITE; PS0156; SSD; 1.
SQ SEQUENCE 1359 AA; 148696 MW; 3225D53D93B768B6 CRC64;

Query Match 0.8%; Score 10; DB 2; Length 1359;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1096 TLLGLLHGLV 1105
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Db 1274 TLLGLLHGLV 1283

Search completed: June 16, 2005, 08:07:59
Job time : 202 secs